



CC CD86 (B7-2) (see AAY95321). The invention relates to a novel strategy for  
 CC inhibiting costimulation by porcine cells of human T cells, with  
 CC particular importance in the context of xenotransplantation of porcine  
 CC organs. Recipients are immunised with hybrid synthetic peptides, such as  
 CC the present peptide, comprising a T cell epitope conjugated to sequences  
 CC of the porcine costimulatory molecules CD80, CD86 or CD40. Peptides that  
 CC induce antibodies specific for regions of costimulatory molecules  
 CC involved in binding to their counter-receptors on human cells are capable  
 CC of blocking the delivery of costimulation. Once the antibody response has  
 CC been induced, the transplanted organ will recall this response due to the  
 CC expression of the costimulatory molecules, thereby sustaining the  
 CC blockade, and providing an endogenous mechanism of costimulatory  
 CC response. The method is useful for improving the tolerance of a host to  
 CC xenografts, particularly porcine pancreatic islet cells. (Updated on 12-  
 CC SEP-2003 to standardise OS field)

CC Sequence 26 AA;

Query Match 100.0%; Score 47; DB 3; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9  
 Db 18 GLVPIHOMS 26

RESULT 2  
 AAY95327  
 ID AAY95327 standard; peptide; 30 AA.

AC AAY95327;  
 XX  
 DT 12-SEP-2003 (revised)  
 DT 25-SEP-2000 (first entry)

XX OVA323-339-pig costimulatory molecule B7-2 epitope hybrid peptide 3.

XX Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;  
 KW xenotransplantation; organ transplant; vaccine; B-cell epitope;  
 KW T-cell epitope; ovalbumin; chicken.

XX Gallus sp.  
 OS Sus scrofa.  
 OS Chimeric.

XX Key Location/Qualifiers  
 FT Peptide 1..17  
 FT /note= "OVA323-339"  
 FT 18..30  
 FT /note= "B7-2 amino acids 109-121"

XX WO20037102-A2.

XX 29-JUN-2000.

XX 17-DEC-1999; 99WO-GB004200.

XX 19-DEC-1998; 98GB-00027921.

XX 23-OCT-1999; 99GB-00025015.

XX (MML-) ML LAB PLC.

XX Lechler RI, Rogers NJ, Dorling A;

XX WPI, 2000-442537/38.

XX Novel methods for improving tolerance to a xenograft comprising  
 PT immunising a mammal with a T-cell epitope and a B-cell epitope.

XX Disclosure: Page 23; 81pp; English.

XX The present sequence is that of chimeric peptide 3 comprising T-cell

CC epitope OVA323-339 from chicken egg albumin (ovalbumin) and a B-cell  
 CC epitope comprising amino acids 109-121 of pig co-stimulatory molecule  
 CC CD86 (B7-2) (see AAY95321). The invention relates to a novel strategy for  
 CC inhibiting costimulation by porcine cells of human T cells, with  
 CC particular importance in the context of xenotransplantation of porcine  
 CC organs. Recipients are immunised with hybrid synthetic peptides, such as  
 CC the present peptide, comprising a T cell epitope conjugated to sequences  
 CC of the porcine costimulatory molecules CD80, CD86 or CD40. Peptides that  
 CC induce antibodies specific for regions of costimulatory molecules  
 CC involved in binding to their counter-receptors on human cells are capable  
 CC of blocking the delivery of costimulation. Once the antibody response has  
 CC been induced, the transplanted organ will recall this response due to the  
 CC expression of the costimulatory molecules, thereby sustaining the  
 CC response, and providing an endogenous mechanism of costimulatory  
 CC blockade. The method is useful for improving the tolerance of a host to  
 CC xenografts, particularly porcine pancreatic islet cells. (Updated on 12-  
 CC SEP-2003 to standardise OS field)

CC Sequence 30 AA;

Query Match 100.0%; Score 47; DB 3; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 0.015;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9  
 Db 22 GLVPIHOMS 30

RESULT 3  
 AAM14944  
 ID AAM14944 standard; protein; 250 AA.

AC AAM14944;  
 XX

DT 17-OCT-2003 (revised)  
 DT 16-JUN-1997 (first entry)

XX Chimeric human/porcine CD86.

XX Xenotransplantation; graft rejection; cell interaction; pig; CD86;  
 KW monoclonal antibody; chimeric antibody; diagnosis.

XX Homo; sapiens.  
 OS Sus scrofa.  
 OS Chimeric.

XX Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /label= Sig\_peptide  
 FT Protein 26..250  
 FT /label= Mat\_protein  
 FT Region 246..250  
 FT /label= Histidine\_tag

XX WO9711971-A1.

XX 03-APR-1997.

XX 27-SEP-1996; 96WO-US015575.

XX 28-SEP-1995; 95US-0004489P.

XX 26-SEP-1996; 96US-00004489.

XX (ALEX-) ALEXION PHARM INC.

XX Mueller JF, Evans MJ, Mueller EE, Rollins S, Rother RP, Mattis LA;

XX WPI, 1997-212855/19.

XX N-PSDB; AAT62939.

XX Antibodies binding to porcine but not human cell interaction proteins -  
 PT useful to treat and assay for rejection of xenografted porcine organs,

| FT       | ttissues or cells.                                                        |
|----------|---------------------------------------------------------------------------|
| PS       | Disclosure; Page 69-70; 105pp; English.                                   |
| XX       |                                                                           |
| CC       | A chimeric human/porcine CD86 (B7-2) cell adhesion molecule has amino     |
| CC       | acid residues 1-4 and 197-245 from human CD86, and amino acids 5-196 from |
| CC       | porcine CD86. It is encoded by a DNA construct (AA62939) obt'd. by PCR    |
| CC       | amplification of porcine sequences and ligation to a sequence encoding    |
| CC       | the C-terminal region of human CD86 19C domain. A signal sequence         |
| CC       | facilitates efficient secretion from transfected mammalian cells.         |
| CC       | Antibodies to porcine CD86 protein, P-selectin (see also AA61945) and     |
| CC       | vascular cell adhesion molecule (see also AA614931-42) are useful for     |
| CC       | diagnosing human rejection of porcine xenotransplants and for improving   |
| CC       | xenotransplantation of porcine cells, tissues and organs into human       |
| CC       | recipients. (Updated on 17-OCT-2003 to standardise OS field)              |
| XX       |                                                                           |
| SO       | Sequence 250 AA.                                                          |
| QY       | Query Match 100.0%; Score 47; DB 2; Length 250;                           |
| DB       | Best Local Similarity 100.0%; Pred. No. 0.17;                             |
|          | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0                 |
|          | 1 GLVPIHOMS 9                                                             |
|          |                                                                           |
| DB       | 119 GLVPIHOMS 127                                                         |
| RESULT 4 |                                                                           |
| AA95321  |                                                                           |
| ID       | AA95321 standard; protein; 325 AA.                                        |
| XX       |                                                                           |
| AC       | AA95321;                                                                  |
| XX       |                                                                           |
| DT       | 25-SEP-2000 (first entry)                                                 |
| XX       |                                                                           |
| DE       | Pig costimulatory molecule CD86 (B7-2).                                   |
| XX       |                                                                           |
| KM       | Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;              |
| KW       | Xenotransplantation; organ transplant; vaccine; epitope.                  |
| XX       |                                                                           |
| OS       | Sus scrofa.                                                               |
| XX       |                                                                           |
| FT       | Key Location/Qualifiers                                                   |
| FT       | Peptide 17..29 "peptide 9"                                                |
| FT       | /note="peptide 9"                                                         |
| FT       | Peptide 21..32                                                            |
| FT       | /note="peptide 8"                                                         |
| FT       | Peptide 32..40                                                            |
| FT       | /note="peptide 2"                                                         |
| FT       | Peptide 76..88 "peptide 10"                                               |
| FT       | /note="peptide 10"                                                        |
| FT       | Peptide 81..90                                                            |
| FT       | /note="peptide 1"                                                         |
| FT       | Peptide 94..104                                                           |
| FT       | /note="peptide 5"                                                         |
| FT       | Peptide 109..121                                                          |
| FT       | /note="peptide 3"                                                         |
| FT       | Peptide 113..121                                                          |
| FT       | /note="peptide 4"                                                         |
| FT       | Peptide 151..162                                                          |
| FT       | /note="peptide 6"                                                         |
| XX       |                                                                           |
| PN       | W0300037102-A2.                                                           |
| XX       |                                                                           |
| PD       | 29-JUN-2000.                                                              |
| XX       |                                                                           |
| PF       | 17-DEC-1999; 99MO-GB004200.                                               |
| XX       |                                                                           |
| PR       | 19-DEC-1998; 98GB-00027921.                                               |
| PR       | 23-OCT-1999; 99GB-00025015.                                               |
| XX       |                                                                           |
| PA       | (MIML-) ML LAB PLC.                                                       |
| XX       |                                                                           |

|                       |                                                                           |
|-----------------------|---------------------------------------------------------------------------|
| PI                    | Lechler R1, Rogers NT, Dörling A;                                         |
| XX                    |                                                                           |
| DR                    | WPI: 2000-442537/38.                                                      |
| DR                    | N-PSDB: AAA49661.                                                         |
| XX                    |                                                                           |
| PT                    | Novel methods for improving tolerance to a xenograft comprising           |
| PT                    | immunizing a mammal with a T-cell epitope and a B-cell epitope.           |
| XX                    |                                                                           |
| PS                    | Disclosure; Fig 6; 81pp; English.                                         |
| XX                    |                                                                           |
| CC                    | The present sequence is that of pig co-stimulatory molecule CD86 (B7-2),  |
| CC                    | as deduced from an isolated cDNA clone (see AAA49661). CD86 plays a key   |
| CC                    | role in T cell costimulation. The invention relates to a novel strategy   |
| CC                    | for inhibiting costimulation by porcine cells of human T cells, with      |
| CC                    | particular importance in the context of xerotransplantation of porcine    |
| CC                    | organs. Recipients are immunised with hybrid synthetic peptides           |
| CC                    | comprising a T cell epitope conjugated to sequences of the porcine        |
| CC                    | costimulatory molecules CD80, CD86 or CD40, such as peptides 1-10 of CD86 |
| CC                    | (see also AA95325-33). Peptides that induce antibodies specific for       |
| CC                    | regions of costimulatory molecules involved in binding to their counter-  |
| CC                    | receptors on human cells (CD28 and CD14) are capable of blocking the      |
| CC                    | delivery of costimulation. Once the antibody response has been induced,   |
| CC                    | the transplanted organ will recall this response due to the expression of |
| CC                    | the costimulatory molecules, thereby sustaining the response, and         |
| CC                    | providing an endogenous mechanism of costimulatory blockade. The method   |
| CC                    | is useful for improving the tolerance of a host to xenografts,            |
| CC                    | particularly porcine pancreatic islet cells                               |
| XX                    |                                                                           |
| SO                    | Sequence 325 AA;                                                          |
| XX                    |                                                                           |
| Query Match           | 100.0%; Score 47; DB 3; Length 325;                                       |
| Best Local Similarity | 100.0%; Pred. No. 0.23;                                                   |
| Matches               | 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                        |
| OY                    | 1 GLVPIHOMS 9                                                             |
|                       |                                                                           |
|                       | 113 GLVPIHOMS 121                                                         |
| Db                    |                                                                           |
| XX                    |                                                                           |
| RESULT 5              |                                                                           |
| ID                    | AA95324                                                                   |
| AA95324               | standard; protein: 325 AA.                                                |
| XX                    |                                                                           |
| AC                    | AA95324;                                                                  |
| XX                    |                                                                           |
| DT                    | 25-SEP-2000 (first entry)                                                 |
| XX                    |                                                                           |
| DE                    | Human costimulatory molecule CD86 (B7-2).                                 |
| XX                    |                                                                           |
| KM                    | Co-stimulatory molecule; CD86; B7-2; human; immunosuppressive;            |
| KM                    | xerotransplantation; organ transplant; vaccine; epitope.                  |
| XX                    |                                                                           |
| OS                    | Homo sapiens.                                                             |
| XX                    |                                                                           |
| FT                    | Key                                                                       |
| FT                    | Peptide                                                                   |
| FT                    | Location/Qualifiers                                                       |
| FT                    | 19..42                                                                    |
| FT                    | /note= "epitope"                                                          |
| FT                    | 53..73                                                                    |
| FT                    | /note= "epitope"                                                          |
| FT                    | 101..129                                                                  |
| FT                    | /note= "epitope"                                                          |
| FT                    | 136..165                                                                  |
| FT                    | /note= "epitope"                                                          |
| XX                    |                                                                           |
| FN                    | WO200037102-A2.                                                           |
| XX                    |                                                                           |
| PD                    | 29-JUN-2000.                                                              |
| XX                    |                                                                           |
| PF                    | 17-DEC-1999; 99WO-GB004200.                                               |
| XX                    |                                                                           |
| PR                    | 19-DEC-1998; 98GB-00027921.                                               |
| XX                    |                                                                           |
| PR                    | 23-OCT-1999; 99GB-00025015.                                               |
| XX                    |                                                                           |

|          |                                                                           |
|----------|---------------------------------------------------------------------------|
| XX       | (MMLT-) ML LAB PLC.                                                       |
| PA       | Lechler RI, Rogers NU, Dorling A;                                         |
| PI       | WPI; 2000-442537/38.                                                      |
| DR       |                                                                           |
| XX       | Novel methods for improving tolerance to a xenograft comprising           |
| PT       | immunizing a mammal with a T-cell epitope and a B-cell epitope.           |
| XX       |                                                                           |
| PS       | Disclosure; Fig 26; 81pp; English.                                        |
| XX       |                                                                           |
| CC       | The present sequence is that of human co-stimulatory molecule CD86 (B7-   |
| CC       | 2). CD86 plays a key role in T cell costimulation. The invention relates  |
| CC       | to a novel strategy for inhibiting costimulation by porcine cells of      |
| CC       | human T cells, with particular importance in the context of               |
| CC       | xenotransplantation of porcine organs. Recipients are immunised with      |
| CC       | hybrid synthetic peptides comprising a T cell epitope conjugated to       |
| CC       | sequences of the porcine costimulatory molecules CD80, CD86 or CD40 (see  |
| CC       | AAV95321-24). Peptides that induce antibodies specific for regions of     |
| CC       | costimulatory molecules involved in binding to their counter-receptors on |
| CC       | human cells (CD28 and CD14) are capable of blocking the delivery of       |
| CC       | costimulation. Once the antibody response has been induced, the           |
| CC       | transplanted organ will recall this response due to the expression of the |
| CC       | costimulatory molecules, thereby sustaining the response, and providing   |
| CC       | an endogenous mechanism of costimulatory blockade. The method is useful   |
| CC       | for improving the tolerance of a host to xenografts, particularly porcine |
| CC       | pancreatic islet cells                                                    |
| CC       |                                                                           |
| XX       |                                                                           |
| SQ       | Sequence 325 AA;                                                          |
|          |                                                                           |
|          | Query Match 100.0%; Score 47; DB 3; Length 325;                           |
|          | Best Local Similarity 100.0%; Pred. No. 0.23;                             |
|          | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.                |
| Oy       | 1 GLVPFHOMS 9<br>   <br>                                                  |
| Db       | 113 GLVPFHOMS 121                                                         |
|          |                                                                           |
| RESULT 6 |                                                                           |
| AAV32278 |                                                                           |
| ID       | AAV32278 standard; protein; 329 AA.                                       |
| XX       |                                                                           |
| AC       | AAV32278;                                                                 |
| XX       |                                                                           |
| DT       | 12-SEP-2003 (revised)                                                     |
| DT       | 15-FEB-2000 (first entry)                                                 |
| XX       |                                                                           |
| DE       | Cat CD86 (B7-2) ligand.                                                   |
| XX       |                                                                           |
| CM       | CD86: B7-2; ligand; cat; vaccine; feline immunodeficiency virus; FIV;     |
| KW       | feline leukemia virus; feline infectious peritonitis virus;               |
| KW       | feline panleukopenia virus; feline calicivirus; feline reovirus-3;        |
| KW       | feline rotavirus; feline coronavirus; feline syncytial virus;             |
| KW       | feline sarcoma virus; feline herpesvirus; feline borna disease;           |
| KW       | rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;       |
| KW       | pasteite; autoimmune disease; transplant rejection; therapy.              |
| XX       |                                                                           |
| OS       | Felis catus.                                                              |
| XX       |                                                                           |
| PN       | MO9957271-A2.                                                             |
| XX       |                                                                           |
| PD       | 11-NOV-1999.                                                              |
| XX       |                                                                           |
| PF       | 30-APR-1999; 99WO-US009502.                                               |
| XX       |                                                                           |
| PR       | 01-MAY-1998; 98US-00071699.                                               |
| XX       |                                                                           |
| PA       | (TEXA ) TEXAS A & M SYSTEM.                                               |
| XX       |                                                                           |
| FI       | Collison EW, Hash SM, Choi I;                                             |
| XX       |                                                                           |
| DR       | WPI; 2000-052972/04.                                                      |

|                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
|-----------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| DR                    | N-PSDB; AA234785.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| XX                    | Novel feline proteins used to produce feline vaccines which prevent infectious disease or to promote growth in homologous or heterologous species.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| XX                    | Example 1A; Fig 3A; 186pp; English.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| XX                    | The present sequence represents feline CD86 (B7-2) ligand, as predicted from isolated cDNA of peripheral blood mononuclear cells. The coexpression of CD86 with the costimulatory molecules CD28 (see AAY32279) and a tumour antigen or an antigen from a pathogenic organism has the ability to activate or enhance activation of T-lymphocytes. Coexpression of CD86 with CTLA-4 (see AAY32280) has the ability to regulate activation of T-lymphocytes. The invention provides isolated nucleic acids encoding feline CD86 ligand, feline CD80 (B7-1) ligand, feline CD28 receptor or feline CTLA-4 (CD152) receptor, as well as vectors comprising the nucleic acids, and polypeptides encoded by the nucleic acids. It also provides vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and further comprising immunogens derived from pathogens, especially feline immunodeficiency virus (FIV), feline leukaemia virus, feline infectious peritonitis virus, feline panleukopenia virus, feline calicivirus, feline reovirus-3, feline rotavirus, feline coronavirus, feline syncytial virus, feline sarcoma virus, feline herpesvirus, feline borra disease virus, rabies virus, chlamydia, Toxoplasmosis gondii, Dirofilaria immitis, or a flea, bacterial pathogen, or parasite (all claimed). |
| CC                    | Vaccines capable of enhancing an immune response, and vaccines capable of suppressing an immune response (suitable for treating an autoimmune disease or tissue or organ transplant rejection) are claimed. (Updated on 12-Sep-2003 to standardise OS field)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| XX                    | Sequence 329 AA;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| SQ                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| Query Match           | 93.6%; Score 44; DB 3; Length 329;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| Best Local Similarity | 88.9%; Pred.No. 1;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| Matches               | 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| CY                    | 1 GIYPIHQMS 9<br>   :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Db                    | 120 GLVPHQMS 128                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| RESULT 7              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| AAY32285              | AA32285 strand; protein; 329 AA.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| XX                    | AA32285;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| AC                    | 12-SEP-2003 (revised)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| DT                    | 28-FEB-2000 (first entry)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| XX                    | Feline CD86 (B7-2).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| DE                    | CD86; B7-2; feline; cat; recombinant virus; vaccine; immunomodulator; tumour; cancer; therapy.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| KM                    | Felis catus.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| OS                    | MO9957295-A1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| FN                    | WO9957295-A1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| PD                    | 11-NOV-1999.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| XX                    | 30-APR-1999; 99WO-US009504.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| XX                    | 01-MAY-1998; 98US-00071711.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| PR                    | (SCHE ) SCHERING-PLOUGH LTD.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| PA                    | (SCHE ) SCHERING-PLOUGH VETERINARY CORP.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| XX                    | Winslow BJ, Cochran MD;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| XX                    | WPI; 2000-062155/05.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| DR                    | N-PSDB; AA234838.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |

XX Novel recombinant virus useful as immunomodulators, particularly in  
PT vaccines.  
XX  
XX Disclosure; Fig 3A; 230pp; English.  
XX  
CC This sequence represents feline CD86 (B7-2), as deduced from peripheral  
CC blood mononuclear cell cDNA (see A234835). Manipulating the expression  
CC of CD28 or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)  
CC regulates T cell proliferation and cytokine release. The invention  
CC relates to a recombinant virus that contains at least one foreign nucleic  
CC acid, inserted into a nonessential genomic region, that encodes feline  
CC CD28, CD80, CD86 or CTLA-4 protein, or their immunogenic fragments, and  
CC is expressed when the recombinant virus is introduced into a suitable  
CC host. The invention also provides a recombinant virus further comprising  
CC a foreign nucleic acid encoding an immunogen derived from a feline  
CC pathogen; recombinant viruses capable of enhancing an immune response to  
CC protect against disease; recombinant viruses expressing antisense  
CC sequences, capable of suppressing an immune response in a feline, e.g.  
CC for treatment of autoimmune disease or transplant rejection; and  
CC recombinant viruses expressing DNA encoding CD80 and/or CD86 used to  
CC reduce or eliminate a tumour in cats. (Updated on 12-SEP-2003 to  
CC standardise OS field)  
CC  
XX  
SQ Sequence 329 AA;  
  
Query Match 93.6%; Score 44; DB 3; Length 329;  
Best Local Similarity 88.9%; Pred. No. 1;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GLVPIHQMS 9  
|||:||||  
Db 120 GLVPMHQMS 128  
  
RESULT 8  
AA017734  
ID AA017734 standard; protein; 329 AA.  
XX  
AC AA017734;  
XX  
DT 08-AUG-2002 (first entry)  
XX  
DE Feline CD86.  
XX  
XX Cat; CD28; CD80; CTLA-4; CD86; immunogen; vaccine; viral infection;  
XX feline immunodeficiency disease; feline infectious peritonitis;  
XX feline leukemia virus; cancer; degenerative disease; autoimmune disease;  
XX virucide; immunomodulator; cytostatic; immunodeficiency.  
XX  
XX Felis catus.  
XX  
XX US2002051792-A1.  
XX  
XX PD 02-MAY-2002.  
XX  
XX PF 30-APR-1999; 99US-00303040.  
XX  
XX PR 01-MAY-1998; 98US-0083870P.  
XX  
XX (WINS/) WINSLOW B J.  
XX (COCH/) COCHRAN M D.  
XX  
XX Winslow BJ, Cochran MD;  
XX  
XX WPI; 2002-415200/44.  
XX DR N-PSDB; AAL46840.  
XX  
PT New recombinant virus, useful for immunizing felines to prevent or treat  
PT feline immunodeficiency virus, comprises foreign nucleic acid encoding  
PT feline cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or  
PT CTLA-4.  
XX

P5 Disclosure; Fig 3; 77pp; English.  
XX  
CC The present invention relates to a recombinant virus comprising at least  
CC one foreign nucleic acid encoding a protein selected from feline  
CC cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or CTLA-4,  
CC which is capable of expression when the virus is introduced into an  
CC appropriate host. The virus can be administered to the feline in order to  
CC elicit or enhance an immune response to prevent or treat feline  
CC immunodeficiency disease, feline leukemia, feline infectious peritonitis,  
CC cancers, degenerative and autoimmune diseases and immunodeficiency. The  
CC present sequence is a cytotoxic T lymphocyte accessory molecule described  
CC in the exemplification of the invention  
XX  
SQ Sequence 329 AA;  
  
Query Match 93.6%; Score 44; DB 5; Length 329;  
Best Local Similarity 88.9%; Pred. No. 1;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GLVPIHQMS 9  
|||:||||  
Db 120 GLVPMHQMS 128  
  
RESULT 9  
AAU78121  
ID AAU78121 standard; protein; 329 AA.  
XX  
AC AAU78121;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Feline CD86 protein.  
XX  
XX Cat; vaccine; feline immunodeficiency virus; FIV; immunosuppressant;  
XX feline infectious peritonitis; CD80 ligand; CD86 ligand; CD28; receptor;  
XX CTLA-4; vaccine; rabies; autoimmune disease; organ transplant;  
XX toxoplasmosis gondii; flea; parasite; panleukopenia; feline leukemia;  
XX Feline; calicivirus; rotavirus; reovirus type 3; coronavirus; herpes;  
XX borna disease.  
XX  
XX Felis sp.  
XX  
XX US2002028208-A1.  
XX  
XX PD 07-MAR-2002.  
XX  
XX PF 30-APR-1999; 99US-00303510.  
XX  
XX PR 01-MAY-1998; 98US-0083869P.  
XX  
XX (COLL/) COLLISSON E W.  
XX (HASH/) HASH S M.  
XX (CHOI/) CHOI I.  
XX  
XX Collisson EW, Hash SM, Choi I;  
XX  
XX WPI; 2002-315045/35.  
XX DR N-PSDB; ABX48230.  
XX  
XX Polynucleotide encoding polypeptide of CD80 ligand, CD86 ligand, CD28  
XX receptor or CTLA-4 receptor as vaccine for inducing immune response in  
XX feline suffering from autoimmune disease or tissue or organ transplant.  
XX  
XX Disclosure; Fig 3A; 73pp; English.  
XX  
XX This invention relates to the DNA and protein sequences encoding a  
XX soluble CD80 ligand, soluble CD86 ligand, soluble and membrane-bound CD28  
XX receptor and soluble or membrane bound CTLA-4 receptor. The invention  
XX also relates to a vaccine comprising an effective amount of these  
XX receptor proteins. A vaccine is useful for inducing immunity or enhancing  
XX an immune response in a cat. The protein sequences of the invention are  
XX useful for suppressing an immune response in a feline suffering from an

CC autoimmune disease or the recipient of a tissue or organ transplant. A  
 CC vector containing an immune response in a feline to an immunogen such as rabies  
 CC virus, chlamydia, toxoplasmosis gondii, flea, feline immunodeficiency  
 CC virus, feline leukemia virus (FeLV), feline infectious peritonitis virus  
 CC (FIP), parvovirus, calicivirus, reovirus type 3, rotavirus,  
 CC coronavirus, syncytial virus, herpes virus, sarcoma virus, borna disease  
 CC virus or a parasite. The protein sequences may be further utilized to  
 CC promote growth in homologous or heterologous feline species. Enhancement  
 CC of immunity through the interaction of soluble CD80 or soluble CD86 with  
 CC CD28 or CTLA-4 or inhibition of an immune response through the  
 CC interaction of feline CD80 or CD86 with CTLA-4 takes advantage of the  
 CC natural process of regulation rather than adding foreign substances that  
 CC could have multiple, even detrimental effects on overall or long term  
 CC health. The present sequence represents feline CD86 protein of the  
 CC invention

CC Sequence 329 AA;

Query Match 93.6%; Score 44; DB 5; Length 329;  
 Best Local Similarity 88.9%; Pred. No. 1;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIVPIHOMS 9  
 |||||  
 DB 120 GLVPMHOMS 128

RESULT 10

AAV41079 standard; protein; 332 AA.

AAV41079;

20-DEC-1999 (first entry)

Feline B7-2 protein.

B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;

allergic reaction; infectious disease; tumor development; feline;

graft rejection; inflammation; arthritis; atopic dermatitis; se.

Felis catus.

WO9947558-A2.

19-MAR-1999; 99WO-US006187.

19-MAR-1998; 98US-0078765P.

17-APR-1998; 98US-00062597.

(HESK-) HESKA CORP.

Sim G, Yang S, Sellins KS;

WPI; 1999-571822/48.

N-PSDB; AA227923; AA227931.

New isolated B7 and CTLA4 nucleic acids, used to develop products for

treating, e.g. autoimmune and atopic diseases.

Claim 4; Page 116-119; 148pp; English.

CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)  
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be  
 CC expressed by standard recombinant methodology. The nucleic acid molecules  
 CC and the encoded proteins can be used for preventing or treating diseases,  
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor  
 CC development, graft rejection, inflammation, arthritic and atopic diseases  
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,  
 CC cats, cattle, sheep or pets. The products can also be used for detection.

CC diagnosis and drug screening  
 XX Sequence 332 AA;

Query Match

Best Local Similarity 93.6%; Score 44; DB 2; Length 332;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIVPIHOMS 9  
 |||||  
 DB 120 GLVPMHOMS 128

RESULT 11

AAV41078 standard; protein; 280 AA.

AAV41078;

20-DEC-1999 (first entry)

Canine B7-2S protein.

B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;

allergic reaction; infectious disease; tumor development; canine;

graft rejection; inflammation; arthritis; atopic dermatitis.

Canis familiaris.

WO9947558-A2.

19-MAR-1999; 99WO-US006187.

19-MAR-1998; 98US-0078765P.

17-APR-1998; 98US-00062597.

(HESK-) HESKA CORP.

Sim G, Yang S, Sellins KS;

WPI; 1999-571822/48.

N-PSDB; AA227921; AA227923.

New isolated B7 and CTLA4 nucleic acids, used to develop products for

treating, e.g. autoimmune and atopic diseases.

Claim 4; Page 109-111; 148pp; English.

CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)  
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be  
 CC expressed by standard recombinant methodology. The nucleic acid molecules  
 CC and the encoded proteins can be used for preventing or treating diseases,  
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor  
 CC development, graft rejection, inflammation, arthritic and atopic diseases  
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,  
 CC cats, cattle, sheep or pets. The products can also be used for detection,  
 CC diagnosis and drug screening

Sequence 280 AA;

Query Match 87.2%; Score 41; DB 2; Length 280;  
 Best Local Similarity 77.8%; Pred. No. 3; 6;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIVPIHOMS 9  
 |||||  
 DB 119 GLVPMHOMS 127

RESULT 12

AAV41076

```

ID AA41076 standard; protein; 329 AA.
XX
XX AA41076;
AC
XX
XX 20-DEC-1999 (first entry)
DE
XX Canine B7-2 protein.
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; canine;
XX graft rejection; inflammation; arthritis; atopic dermatitis.
XX
XX Canis familiaris.
OS
XX WO947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US006187.
XX
XX 19-MAR-1998; 98US-0078765P.
XX
XX 17-APR-1998; 98US-00062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI; 1999-571822/48.
XX
XX N-PSDB; AA227913, AA227915.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases.
XX
XX Claim 4; Page 97-99; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritis and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening
XX
XX Sequence 329 AA;
SQ
Query Match 87.2%; Score 41; DB 2; Length 329;
Best Local Similarity 77.8%; Pred. No. 4.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLVPIHQMS 9
Db 119 GLVPIHQMN 127

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PN WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
XX
XX 02-JUN-2000; 2000US-0208841P.
XX
XX 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI; 2001-616774/71.
XX
XX N-PSDB; AAS59513.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
XX vaccinating against and diagnosing infections, especially useful for
XX treating acne vulgaris.
XX
XX Example 1; SEQ ID NO 2158; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX polypeptides. The proteins and their associated DNA sequences are used in
XX the treatment, prevention and diagnosis of medical conditions caused by
XX P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
XX P. acnes is also involved in infections of bone, joints and the central
XX nervous system, however it is particularly involved in the inflammatory
XX lesions associated with acne vulgaris. A method for detecting the
XX presence or absence of P. acnes in a patient comprises contacting a
XX sample with a binding agent that binds to the proteins of the invention
XX and determining the amount of bound protein in the sample. The
XX polypeptides may be used as antigens in the production of antibodies
XX specific for P. acnes proteins. These antibodies can be used to
XX downregulate expression and activity of P. acnes polypeptides and
XX therefore treat P. acnes infections. The antibodies may also be used as
XX diagnostic agents for determining P. acnes presence, for example, by
XX enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 303 AA;
SQ
Query Match 80.9%; Score 38; DB 4; Length 303;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLVPIHQMS 9
Db 35 GIAPIHQLS 43

```

```

RESULT 13
AAU40963
ID AAU40963 standard; protein; 303 AA.
XX
XX AAU40963;
AC
XX
XX 13-FEB-2002 (first entry)
XX
XX Propionibacterium acnes immunogenic protein #1859.
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX dermatological; osteopathic; neuroprotectant.
XX
XX Propionibacterium acnes.
XX
XX

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```

RESULT 14
ABM37482
ID ABM37482 standard; protein; 303 AA.
XX
XX ABM37482;
AC
XX
XX 20-OCT-2003 (first entry)
XX
XX Propionibacterium acnes predicted ORF-encoded polypeptide #2158.
XX
XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX immunostimulant; immune response; vaccine.
XX
XX Propionibacterium acnes.
XX
XX WO2003033515-A1.
XX
XX

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|                                                                       |                                                                           |
|-----------------------------------------------------------------------|---------------------------------------------------------------------------|
| PD                                                                    | 24-APR-2003.                                                              |
| PE                                                                    | 11-OCT-2002; 2002MO-US032727.                                             |
| PR                                                                    | 15-OCT-2001; 2001US-00978825.                                             |
| PA                                                                    | (CORI-) CORIXA CORP.                                                      |
| P1                                                                    | Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;             |
| P2                                                                    | Mang S, Jen S, Lodes MJ, Benson DE, Jones R, Carter D,                    |
| P3                                                                    | Barth B, Vallilve-Douglase J;                                             |
| DR                                                                    | WP1; 2003-381789/36.                                                      |
| DS                                                                    | N-PSDB; ACP64442.                                                         |
| PT                                                                    | New Propionibacterium acnes polypeptides and polynucleotides encoding the |
| PI                                                                    | polypeptide, useful for diagnosing, preventing or treating acne vulgaris, |
| PN                                                                    | or for stimulating an immune response specific for a P. acnes protein.    |
| PS                                                                    | Example 1; SEQ ID NO 2158; 1481bp; English.                               |
| XX                                                                    | The invention relates to an isolated polynucleotide (ACF64435-ACF64733)   |
| CC                                                                    | encoding a Propionibacterium acnes protein. The invention also relates to |
| CC                                                                    | polypeptides encoded by the polynucleotides (AM365624-AM64536) and to     |
| CC                                                                    | immunogenic fragments of P. acnes polypeptides. The invention             |
| CC                                                                    | additionally encompasses expression vectors and host cells comprising a   |
| CC                                                                    | polynucleotide of the invention; antibodies against polypeptides of the   |
| CC                                                                    | invention; fusion proteins comprising a polypeptide of the invention; a   |
| CC                                                                    | method for stimulating an immune response specific for a P. acnes         |
| CC                                                                    | polypeptide and an isolated T cell population comprising T cells prepared |
| CC                                                                    | via this method; a vaccine composition (comprising P. acnes polypeptides, |
| CC                                                                    | polynucleotides, antibodies, fusion proteins, T cell populations, or      |
| CC                                                                    | antigen-presenting cells that express the polypeptide); a method and kit  |
| CC                                                                    | for detecting or determining the presence or absence of P. acnes in a     |
| CC                                                                    | patient; and a method for inhibiting the development of P. acnes in a     |
| CC                                                                    | patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion   |
| CC                                                                    | proteins, T cell populations or antigen-presenting cells that express the |
| CC                                                                    | polypeptides are useful for diagnosing, preventing or treating acne       |
| CC                                                                    | vulgaris, or for stimulating an immune response specific for a P. acnes   |
| CC                                                                    | vulgaris. The polynucleotides can also be used as probes or primers for   |
| CC                                                                    | nucleic acid hybridisation. The vaccine composition is useful for the     |
| CC                                                                    | stimulation of an immune response against P. acnes, or for treating acne, |
| CC                                                                    | and the kit is useful for performing a diagnostic assay. The present      |
| CC                                                                    | sequence represents a polypeptide predicted to be encoded by an ORF (open |
| CC                                                                    | reading frame) contained within the P. acnes polynucleotides of the       |
| CC                                                                    | invention. Note: The sequence data for this patent did not form part of   |
| CC                                                                    | the printed specification, but was obtained in electronic format directly |
| CC                                                                    | from WIPO at ftp.wipo.int/pub/published_pct_sequences                     |
| XX                                                                    | SEQ                                                                       |
| SQ                                                                    | Sequence 303 AA;                                                          |
| Query Match                                                           | 80.9%; Score 36; DB 6; Length 303;                                        |
| Best Local Similarity                                                 | 66.7%; Pred. No. 17;                                                      |
| Matches                                                               | 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;                        |
| Qy                                                                    | 1 GLVPIHQMS 9                                                             |
| Dd                                                                    | :         :                                                               |
|                                                                       | 35 GIAPHHQLS 43                                                           |
| RESULT 15                                                             |                                                                           |
| ID                                                                    | ABO79571 standard; protein; 103 AA.                                       |
| ABO79571                                                              |                                                                           |
| AC                                                                    | ABO79571;                                                                 |
| DT                                                                    | 29-JUL-2004 (first entry)                                                 |
| DE                                                                    | Pseudomonas aeruginosa polypeptide #11746.                                |
| Bacterial infection; Pseudomonas aeruginosa infection; antibacterial. |                                                                           |
| Pseudomonas aeruginosa.                                               |                                                                           |

```

XX  US6551795-B1.
PM
XX
XX  22-APR-2003.
ED
XX
XX  18-FEB-1999; 99US-00252991.
PF
XX
XX  18-FEB-1998; 98US-0074788P.
PR
XX  27-JUL-1998; 98US-0094190C.
PR
XX
XX  (GENO-) GENOME THERAPEUTICS CORP.
PA
XX
XX  Rubenfield MJ, Nolling J, DeLoughery C, Bush D;
PI
XX
XX  WPI: 2003-615309/58.
DR
XX  N-PSDE; ABD131142.
DR
XX
XX  Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT
XX  useful as molecular targets for diagnostics, prophylaxis and treatment of
PT
XX  pathological conditions resulting from bacterial infection.
XX
XX  Disclosure; SEQ ID NO 28317; 455BP; English.
PS
XX
XX  The invention relates to Pseudomonas aeruginosa polypeptides and the
XX  polynucleotides encoding them. The sequences are useful in diagnosis and
XX  therapy of pathological conditions, as molecular targets for diagnostics,
XX  prophylaxis and treatment of pathological conditions resulting from a
XX  bacterial infection, for evaluating a compound, such as a polypeptide,
XX  for the ability to bind a P. aeruginosa nucleic acid, as components of
XX  effective antibacterial targets, as targets for antibacterial drugs,
XX  including anti-P. aeruginosa drugs, as templates for recombinant
XX  production of P. aeruginosa-derived peptides or polypeptides, as target
XX  components for diagnosis and/or treatment of P. aeruginosa-caused
XX  infection, and in detection of P. aeruginosa sequences or other sequences
XX  of Pseudomonas species using diocrypt technology. Sequences ABO67826-
XX  ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
XX  sequence data for this patent did not form part of the printed
XX  specification but was obtained in electronic format from USPTO at
XX  seqdata.uspto.gov/sequence.html
XX
XX  Sequence 103 AA:
SQ
XX
XX  Query Match 78.7%; Score 37; DB 7; Length 103;
XX  Best Local Similarity 66.7%; Pred. No. 8.1;
XX  Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0
XX
XX  1 GLVPIHQMS 9
XX  |||||::
XX  61 GLPIHQIA 69

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:29:06 ; Search time 15.4286 Seconds

(without alignments)  
38.685 Million cell updates/sec

Title: US-09-868-605-14\_COPY\_113\_121

Perfect score: 47

Sequence: 1 GLVPIHQM 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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2: /cgn2\_6/prodata/1/iaa/55\_COMB.pep:\*

3: /cgn2\_6/prodata/1/iaa/68\_COMB.pep:\*

4: /cgn2\_6/prodata/1/iaa/68\_COMB.pep:\*

5: /cgn2\_6/prodata/1/iaa/68\_COMB.pep:\*

6: /cgn2\_6/prodata/1/iaa/backfillseq1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID                     | Description       |
|------------|-------|-------------|--------|------------------------|-------------------|
| 1          | 47    | 100.0       | 325    | 4 US-09-651-200-20     | Sequence 20, Appl |
| 2          | 44    | 93.6        | 329    | 4 US-09-651-200-18     | Sequence 18, Appl |
| 3          | 44    | 93.6        | 329    | 4 US-09-303-040-6      | Sequence 6, Appl  |
| 4          | 41    | 87.2        | 329    | 4 US-09-651-200-19     | Sequence 19, Appl |
| 5          | 37    | 78.7        | 103    | 4 US-09-252-991A-28317 | Sequence 28317, A |
| 6          | 34    | 72.3        | 1305   | 3 US-08-864-785-3      | Sequence 3, Appl  |
| 7          | 34    | 72.3        | 1353   | 3 US-08-894-173-2      | Sequence 2, Appl  |
| 8          | 34    | 72.3        | 1353   | 3 US-09-398-193-2      | Sequence 3, Appl  |
| 9          | 34    | 72.3        | 1353   | 3 US-09-473-717-3      | Sequence 3, Appl  |
| 10         | 34    | 72.3        | 1884   | 4 US-09-538-092-1339   | Sequence 1329, Ap |
| 11         | 33    | 70.2        | 249    | 4 US-09-270-767-4436   | Sequence 44136, A |
| 12         | 33    | 70.2        | 275    | 3 US-09-134-001C-3290  | Sequence 3290, Ap |
| 13         | 33    | 70.2        | 496    | 4 US-09-252-991A-31314 | Sequence 31314, A |
| 14         | 33    | 70.2        | 525    | 4 US-09-252-991A-28266 | Sequence 28266, A |
| 15         | 32    | 68.1        | 91     | 4 US-09-621-976-7293   | Sequence 7293, Ap |
| 16         | 32    | 68.1        | 110    | 3 US-08-479-744A-45    | Sequence 45, Appl |
| 17         | 32    | 68.1        | 110    | 3 US-08-280-757B-45    | Sequence 45, Appl |
| 18         | 32    | 68.1        | 110    | 4 US-09-425-762-45     | Sequence 45, Appl |
| 19         | 32    | 68.1        | 229    | 4 US-10-101-664A-553   | Sequence 593, App |
| 20         | 32    | 68.1        | 333    | 4 US-09-651-200-21     | Sequence 21, Appl |
| 21         | 32    | 68.1        | 333    | 4 US-09-441-111-22     | Sequence 22, Appl |
| 22         | 32    | 68.1        | 333    | 5 PCT-US94-09642-2     | Sequence 2, Appl  |
| 23         | 32    | 68.1        | 334    | 4 US-09-910-174B-6     | Sequence 6, Appl  |
| 24         | 32    | 68.1        | 334    | 4 US-09-620-461-6      | Sequence 6, Appl  |
| 25         | 32    | 68.1        | 329    | 4 US-08-456-104-2      | Sequence 2, Appl  |
| 26         | 32    | 68.1        | 329    | 2 US-08-101-624-2      | Sequence 2, Appl  |
| 27         | 32    | 68.1        | 329    | 3 US-08-479-744A-2     | Sequence 2, Appl  |

|    |    |      |     |                        |                   |
|----|----|------|-----|------------------------|-------------------|
| 28 | 32 | 68.1 | 329 | 3 US-08-280-757B-2     | Sequence 2, Appl  |
| 29 | 32 | 68.1 | 329 | 3 US-08-205-687A-23    | Sequence 23, Appl |
| 30 | 32 | 68.1 | 329 | 3 US-08-702-525-23     | Sequence 23, Appl |
| 31 | 32 | 68.1 | 329 | 3 US-08-403-253A-4     | Sequence 4, Appl  |
| 32 | 32 | 68.1 | 329 | 4 US-09-667-115-32     | Sequence 32, Appl |
| 33 | 32 | 68.1 | 329 | 4 US-08-435-816A-4     | Sequence 4, Appl  |
| 34 | 32 | 68.1 | 329 | 4 US-09-425-762-2      | Sequence 2, Appl  |
| 35 | 32 | 68.1 | 329 | 4 US-09-837-867A-23    | Sequence 23, Appl |
| 36 | 32 | 68.1 | 329 | 4 US-09-206-132-23     | Sequence 2, Appl  |
| 37 | 32 | 68.1 | 329 | 4 US-09-441-411-26     | Sequence 26, Appl |
| 38 | 32 | 68.1 | 329 | 5 PCT-US95-02576-23    | Sequence 23, Appl |
| 39 | 32 | 68.1 | 351 | 4 US-09-756-983-18     | Sequence 18, Appl |
| 40 | 32 | 68.1 | 392 | 4 US-09-710-279-1908   | Sequence 1908, Ap |
| 41 | 32 | 68.1 | 392 | 4 US-09-710-279-2758   | Sequence 2758, Ap |
| 42 | 32 | 68.1 | 411 | 3 US-09-134-001C-3121  | Sequence 3121, Ap |
| 43 | 32 | 68.1 | 460 | 4 US-08-543-681A-5773  | Sequence 5773, Ap |
| 44 | 32 | 68.1 | 553 | 4 US-09-252-991A-24465 | Sequence 24465, A |
| 45 | 32 | 68.1 | 872 | 3 US-08-337-797A-2     | Sequence 2, Appl  |

#### ALIGNMENTS

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RESULT 1
US-09-651-200-20
; Sequence 20, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Polypeptide Activation Antigen B-7 Family and
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651.200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 325
; TYPE: PRT
; ORGANISM: sus sp.
US-09-651-200-20
Query Match          100.0%; Score 47; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. NO. 0.051;
Matches          9; Conservative          0; Mismatches          0; Indels          0; Gaps          0;
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QY 1 GLVPIHQM 9  
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DB 113 GLVPIHQM 121

RESULT 2  
US-09-651-200-18  
; Sequence 18, Application US/09651200  
; Patent No. 6429303  
; GENERAL INFORMATION:  
; APPLICANT: Green et al  
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
; TITLE OF INVENTION: Polypeptide Activation Antigen B-7 Family and  
; FILE REFERENCE: 15966-562 (CURA-62)  
; CURRENT APPLICATION NUMBER: US/09/651.200  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/152383  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 60/172909

;; PRIOR FILING DATE: 1999-12-21  
;; PRIOR APPLICATION NUMBER: 60/183578  
;; PRIOR FILING DATE: 2000-02-18  
;; NUMBER OF SEQ ID NOS: 25  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO: 18  
;; LENGTH: 329  
;; TYPE: PRT  
;; ORGANISM: Felis catus  
US-09-651-200-18

Query Match 93.6%; Score 44; DB 4; Length 329;  
Best Local Similarity 88.9%; Pred. No. 0.22;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9  
DB 120 GLVPIHOMS 128

RESULT 3  
US-09-303-040-6  
; Sequence 6, Application US/09303040  
; Patent No. 6555671  
; GENERAL INFORMATION:  
; APPLICANT: Winslow, Barbara J.  
; APPLICANT: Cochran, Mark D.  
; TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding  
; TITLE OF INVENTION: Feline Interferon-gamma And Uses Thereof  
; FILE REFERENCE: 54957-B  
; CURRENT APPLICATION NUMBER: US/09/303,040  
; CURRENT FILING DATE: 1999-04-30  
; EARLIER APPLICATION NUMBER: 60/083,870  
; EARLIER FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 6  
; TYPE: PRT  
; LENGTH: 329  
; ORGANISM: feline CD86  
US-09-303-040-6

Query Match 93.6%; Score 44; DB 4; Length 329;  
Best Local Similarity 88.9%; Pred. No. 0.22;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9  
DB 120 GLVPIHOMS 128

RESULT 4  
US-09-651-200-19  
; Sequence 19, Application US/09651200  
; Patent No. 6429303  
; GENERAL INFORMATION:  
; APPLICANT: Green et al  
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 15966-562 (CURA-62)  
; CURRENT APPLICATION NUMBER: US/09/651,200  
; CURRENT FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/152383  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 60/172909  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 60/183578  
; PRIOR FILING DATE: 2000-02-18  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 19

;; LENGTH: 329  
;; TYPE: PRT  
;; ORGANISM: Canis familiaris  
US-09-651-200-19

Query Match 87.2%; Score 41; DB 4; Length 329;  
Best Local Similarity 77.8%; Pred. No. 0.97;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9  
DB 119 GLVPIHOMS 127

RESULT 5  
US-09-252-991A-28317  
; Sequence 28317, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO: 28317  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-28317

Query Match 78.7%; Score 37; DB 4; Length 103;  
Best Local Similarity 66.7%; Pred. No. 1.8;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9  
DB 61 GLVPIHOMS 69

RESULT 6  
US-08-864-785-3  
; Sequence 3, Application US/08864785A  
; Patent No. 6329566  
; GENERAL INFORMATION:  
; APPLICANT: Kaplan, Joshua M.  
; APPLICANT: Oppenheimer, Allison J.  
; TITLE OF INVENTION: METHODS FOR THE DETECTION, TREATMENT,  
; TITLE OF INVENTION: AND PREVENTION OF NEURODEGENERATION  
; FILE REFERENCE: 00786/353001  
; CURRENT APPLICATION NUMBER: US/08/864,785A  
; CURRENT FILING DATE: 1997-05-29  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 3  
; LENGTH: 1305  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-08-864-785-3

Query Match 72.3%; Score 34; DB 3; Length 1305;  
Best Local Similarity 66.7%; Pred. No. 1.5e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9  
DB 1249 GLVPIHOMS 1257

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RESULT 7
US-08-894-173-2
; Sequence 2, Application US/08894173A
; Patent No. 6090612
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P14716C
; CURRENT APPLICATION NUMBER: US/08/894,173A
; CURRENT FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1353
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; OTHER INFORMATION: HYPOTHETICAL : NO
US-08-894-173-2

Query Match          72.3%; Score 34; DB 3; Length 1353;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPHQMS 9
DB 1249 GVVPOHQLS 1257

RESULT 8
US-09-398-193-2
; Sequence 2, Application US/09398193
; Patent No. 6197581
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P24360-
; CURRENT APPLICATION NUMBER: US/09/398,193
; CURRENT FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1353
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; OTHER INFORMATION: HYPOTHETICAL : NO
US-09-398-193-2

Query Match          72.3%; Score 34; DB 3; Length 1353;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPHQMS 9
DB 1249 GVVPOHQLS 1257

RESULT 9
US-09-473-717-3
; Sequence 3, Application US/09473717
; Patent No. 6372475
; GENERAL INFORMATION:
; APPLICANT: Storm, Daniel R.
; APPLICANT: Hacker, Beth
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; APPLICANT: University of Washington
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; FILE REFERENCE: 44481-5029-01 US
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; CURRENT APPLICATION NUMBER: US/09/473,717
; CURRENT FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: PCT/US98/13541
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/098,559
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,440
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: PRT
; ORGANISM: murine type IX adenylyl cyclase
US-09-473-717-3

Query Match          72.3%; Score 34; DB 3; Length 1353;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPHQMS 9
DB 1249 GVVPOHQLS 1257

RESULT 10
US-09-538-092-1329
; Sequence 1329, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glco, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatVer Version 0.9
; SEQ ID NO 1329
; LENGTH: 1884
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14690
US-09-538-092-1329

Query Match          72.3%; Score 34; DB 4; Length 1884;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPHQMS 9
DB 580 GLVPHQMS 588

RESULT 11
US-09-270-767-44136
; Sequence 44136, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
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SEQ ID NO 44136  
LENGTH: 249  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-09-270-767-44136

Query Match 70.2%; Score 33; DB 4; Length 249;  
Best Local Similarity 75.0%; Pred. No. 35;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LVPIHQS 9  
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DB 7 MWPHTMS 14

RESULT 12  
US-09-134-001C-3290  
Sequence 3290, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lytta Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: GTC-007  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3290  
LENGTH: 275  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3290

Query Match 70.2%; Score 33; DB 3; Length 275;  
Best Local Similarity 71.4%; Pred. No. 39;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPIHQS 9  
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DB 159 VPIHQS 165

RESULT 13  
US-09-252-991A-31314  
Sequence 31314, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 31314  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-31314

Query Match 70.2%; Score 33; DB 4; Length 496;  
Best Local Similarity 55.6%; Pred. No. 78;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHQS 9

DB 250 GLVPIHQA 258  
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RESULT 14  
US-09-252-991A-28266  
Sequence 28266, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 28266  
LENGTH: 525  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-28266

Query Match 70.2%; Score 33; DB 4; Length 525;  
Best Local Similarity 55.6%; Pred. No. 83;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHQS 9  
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DB 288 GLVPIHQA 296

RESULT 15  
US-09-621-976-7293  
Sequence 7293, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jober, S.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 7293  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-621-976-7293

Query Match 68.1%; Score 32; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 17 LVPIHQ 22

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Thu Dec 16 12:21:11 2004

us-09-868-605-14\_copy\_113\_121.rapb

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 15, 2004, 16:37:44 ; Search time 87.4286 Seconds  
(without alignments)  
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Title: US-09-868-605-14\_COPY\_113\_121

Perfect score: 47 GLVPIHOMS 9

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Gapop 10.0, Gapext 0.5

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Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1          | 44    | 93.6        | 329    | 9  | US-09-303-510-6      |
| 2          | 44    | 93.6        | 329    | 9  | US-09-303-040-6      |
| 3          | 44    | 93.6        | 329    | 16 | US-10-790-396-26     |
| 4          | 41    | 87.2        | 280    | 16 | US-10-790-396-17     |
| 5          | 41    | 87.2        | 329    | 16 | US-10-790-396-7      |
| 6          | 37    | 78.7        | 96     | 17 | US-10-425-115-208294 |
| 7          | 37    | 78.7        | 99     | 15 | US-10-389-647-604    |
| 8          | 36    | 76.6        | 122    | 17 | US-10-425-115-321220 |
| 9          | 36    | 76.6        | 261    | 15 | US-10-282-122A-60956 |
| 10         | 36    | 74.6        | 317    | 17 | US-10-739-930-7964   |
| 11         | 34    | 72.3        | 38     | 9  | US-09-864-761-42375  |
| 12         | 34    | 72.3        | 89     | 17 | US-10-425-115-212035 |
| 13         | 34    | 72.3        | 238    | 10 | US-09-935-338-233    |

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|----|----|------|------|----|----------------------|-------------------|
| 14 | 34 | 72.3 | 238  | 15 | US-10-380-430-59     | Sequence 59, Appl |
| 15 | 34 | 72.3 | 254  | 15 | US-10-282-122A-51529 | Sequence 51529, A |
| 16 | 34 | 72.3 | 258  | 16 | US-10-437-963-146161 | Sequence 146161,  |
| 17 | 34 | 72.3 | 299  | 16 | US-10-437-963-156621 | Sequence 156621,  |
| 18 | 34 | 72.3 | 315  | 14 | US-10-156-761-12810  | Sequence 12810, A |
| 19 | 34 | 72.3 | 1305 | 14 | US-10-014-079A-3     | Sequence 3, Appl  |
| 20 | 34 | 72.3 | 1353 | 9  | US-09-751-100B-2     | Sequence 2, Appl  |
| 21 | 34 | 72.3 | 1353 | 13 | US-10-071-123-3      | Sequence 3, Appl  |
| 22 | 34 | 72.3 | 1855 | 15 | US-10-334-143-21     | Sequence 21, Appl |
| 23 | 34 | 72.3 | 1871 | 14 | US-10-144-194A-114   | Sequence 114, App |
| 24 | 34 | 72.3 | 1884 | 16 | US-10-408-765A-283   | Sequence 283, App |
| 25 | 34 | 72.3 | 1906 | 14 | US-10-144-194A-88    | Sequence 88, Appl |
| 26 | 33 | 70.2 | 105  | 16 | US-10-767-701-49861  | Sequence 49861, A |
| 27 | 33 | 70.2 | 105  | 17 | US-10-425-115-288437 | Sequence 288437,  |
| 28 | 33 | 70.2 | 121  | 16 | US-10-437-963-160312 | Sequence 160312,  |
| 29 | 33 | 70.2 | 219  | 14 | US-10-369-493-12135  | Sequence 12135, A |
| 30 | 33 | 70.2 | 228  | 17 | US-10-425-115-344824 | Sequence 344824,  |
| 31 | 33 | 70.2 | 268  | 15 | US-10-282-122A-71160 | Sequence 71160, A |
| 32 | 33 | 70.2 | 280  | 15 | US-10-425-114-67660  | Sequence 67660, A |
| 33 | 33 | 70.2 | 292  | 15 | US-10-425-114-59810  | Sequence 59810, A |
| 34 | 33 | 70.2 | 407  | 14 | US-10-369-493-16591  | Sequence 16591, A |
| 35 | 33 | 70.2 | 411  | 14 | US-10-369-493-582    | Sequence 582, App |
| 36 | 33 | 70.2 | 429  | 15 | US-10-282-122A-73368 | Sequence 73368, A |
| 37 | 33 | 70.2 | 453  | 15 | US-10-282-122A-55853 | Sequence 55853, A |
| 38 | 33 | 70.2 | 453  | 15 | US-10-282-122A-75796 | Sequence 75796, A |
| 39 | 33 | 70.2 | 464  | 15 | US-10-425-114-41890  | Sequence 41890, A |
| 40 | 33 | 70.2 | 556  | 14 | US-10-156-761-9809   | Sequence 9809, Ap |
| 41 | 33 | 70.2 | 557  | 15 | US-10-403-571-54     | Sequence 54, Appl |
| 42 | 33 | 70.2 | 635  | 15 | US-10-282-122A-53309 | Sequence 53309, A |
| 43 | 33 | 70.2 | 718  | 15 | US-10-282-122A-76979 | Sequence 76979, A |
| 44 | 33 | 70.2 | 1181 | 14 | US-10-199-937-139    | Sequence 139, App |
| 45 | 33 | 70.2 | 3583 | 16 | US-10-437-963-125761 | Sequence 125761,  |

ALIGNMENTS

RESULT 1  
US-09-303-510-6  
; Sequence 6, Application US/09303510A  
; Patent No. US20020028208A1  
; GENERAL INFORMATION:  
; APPLICANT: Collisch, Ellen W.  
; APPLICANT: Choi, Insoo  
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline  
; TITLE OF INVENTION: CITLA-4 Nucleic Acid and Polypeptides  
; FILE REFERENCE: 54954  
; CURRENT APPLICATION NUMBER: US/09/303,510A  
; CURRENT FILING DATE: 1999-04-30  
; EARLIER APPLICATION NUMBER: 60/083,969  
; EARLIER FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 329  
; TYPE: PRT  
; ORGANISM: Feline  
US-09-303-510-6  
Query Match 93.6%; Score 44; DB 9; Length 329;  
Best Local Similarity 88.9%; Pred. No. 3;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GLVPIHOMS 9  
DB 120 GLVPIHOMS 128  
RESULT 2  
US-09-303-040-6  
; Sequence 6, Application US/09303040  
; Patent No. US20020051792A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Wanslow, Barbara J.
/ APPLICANT: Cochran, Mark D.
/ TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
/ TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or
/ TITLE OF INVENTION: Feline Interferon-gamma And Uses Thereof
/ FILE REFERENCE: 54957-B
/ CURRENT APPLICATION NUMBER: US/09/303,040
/ CURRENT FILING DATE: 1999-04-30
/ EARLIER APPLICATION NUMBER: 60/083,870
/ EARLIER FILING DATE: 1998-05-01
/ NUMBER OF SEQ ID NOS: 82
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 329
/ TYPE: PRT
/ ORGANISM: Feline CD86
US-09-303-040-6

Query Match          93.6%; Score 44; DB 9; Length 329;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLVPIHOMS 9
Db      120 GLVPIHOMS 128

RESULT 3
US-10-790-396-26
/ Sequence 26, Application US/10790396
/ Publication No. US20040157296A1
/ GENERAL INFORMATION:
/ APPLICANT: Sim, Gek-Kee
/ APPLICANT: Yang, Shumin
/ APPLICANT: Sellins, Karen S.
/ TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
/ FILE REFERENCE: IM-1-CI-PCT
/ CURRENT APPLICATION NUMBER: US/10/790,396
/ CURRENT FILING DATE: 2004-03-01
/ PRIOR APPLICATION NUMBER: US/09/646,561
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 60/078,765
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 09/062,597
/ PRIOR FILING DATE: 1998-04-17
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 26
/ LENGTH: 332
/ TYPE: PRT
/ ORGANISM: Felis catus
US-10-790-396-26

Query Match          93.6%; Score 44; DB 16; Length 332;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLVPIHOMS 9
Db      120 GLVPIHOMS 128

RESULT 4
US-10-790-396-17
/ Sequence 17, Application US/10790396
/ Publication No. US20040157296A1
/ GENERAL INFORMATION:
/ APPLICANT: Sim, Gek-Kee
/ APPLICANT: Yang, Shumin
/ APPLICANT: Sellins, Karen S.
/ TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
```

```
/ TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
/ FILE REFERENCE: IM-1-CI-PCT
/ CURRENT APPLICATION NUMBER: US/10/790,396
/ CURRENT FILING DATE: 2004-03-01
/ PRIOR APPLICATION NUMBER: US/09/646,561
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 60/078,765
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 09/062,597
/ PRIOR FILING DATE: 1998-04-17
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 17
/ LENGTH: 280
/ TYPE: PRT
/ ORGANISM: Canis familiaris
US-10-790-396-17

Query Match          87.2%; Score 41; DB 16; Length 280;
Best Local Similarity 77.8%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLVPIHOMS 9
Db      119 GLVPIHOMS 127

RESULT 5
US-10-790-396-7
/ Sequence 7, Application US/10790396
/ Publication No. US20040157296A1
/ GENERAL INFORMATION:
/ APPLICANT: Sim, Gek-Kee
/ APPLICANT: Yang, Shumin
/ APPLICANT: Sellins, Karen S.
/ TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
/ FILE REFERENCE: IM-1-CI-PCT
/ CURRENT APPLICATION NUMBER: US/10/790,396
/ CURRENT FILING DATE: 2004-03-01
/ PRIOR APPLICATION NUMBER: US/09/646,561
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 60/078,765
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 09/062,597
/ PRIOR FILING DATE: 1998-04-17
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 7
/ LENGTH: 329
/ TYPE: PRT
/ ORGANISM: Canis familiaris
US-10-790-396-7

Query Match          87.2%; Score 41; DB 16; Length 329;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLVPIHOMS 9
Db      119 GLVPIHOMS 127

RESULT 6
US-10-425-115-208294
/ Sequence 208294, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```

FILE OF INVENTION: Plants  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 208294  
LENGTH: 96  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MWT4577\_121557C.1.pap  
US-10-425-115-208294

Query Match 78.7%; Score 37; DB 17; Length 96;  
Best Local Similarity 85.7%; Pred. No. 19;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLVPIHQ 7  
Db 78 GLVPIHQ 84

RESULT 7  
US-10-389-647-604  
Sequence 604, Application US/10389647  
Publication No. US20040033549A1  
GENERAL INFORMATION:  
APPLICANT: GREENBERG, E. Peter  
APPLICANT: SCHUSTER, Martin  
APPLICANT: LOSTROH, Candl  
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA  
FILE REFERENCE: UTZ-038CD  
CURRENT APPLICATION NUMBER: US/10/389,647  
CURRENT FILING DATE: 2003-03-14  
PRIOR APPLICATION NUMBER: 09/653730  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/153022  
PRIOR FILING DATE: 1999-09-03  
NUMBER OF SEQ ID NOS: 710  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 604  
LENGTH: 99  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-10-389-647-604

Query Match 78.7%; Score 37; DB 15; Length 99;  
Best Local Similarity 66.7%; Pred. No. 20;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLVPIHQ 9  
Db 57 GLVPIHQ 65

RESULT 8  
US-10-425-115-321220  
Sequence 321220, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 321220  
LENGTH: 122  
TYPE: PRT

ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1) ..(122)  
OTHER INFORMATION: unsure at all Xaa locations  
FEATURE:  
OTHER INFORMATION: Clone ID: MWT4577\_56018C.1.pap  
US-10-425-115-321220

Query Match 76.6%; Score 36; DB 17; Length 122;  
Best Local Similarity 75.0%; Pred. No. 38;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LVPIHQ 9  
Db 57 LVPIHQ 64

RESULT 9  
US-10-282-122A-60956  
Sequence 60956, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Jiansu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haasbeck, Robert  
APPLICANT: Ohlsen, Karl  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Twick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 60956  
LENGTH: 261  
TYPE: PRT  
ORGANISM: Listeria monocytogenes  
US-10-282-122A-60956

Query Match 76.6%; Score 36; DB 15; Length 261;  
Best Local Similarity 66.7%; Pred. No. 85;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLVPIHQ 9





```
RESULT 13
US-09-935-338-233
; Sequence 233, Application US/09935338
; Publication No. US20030073081A1
; GENERAL INFORMATION:
; APPLICANT: MIYAKI, Hiroyuki
; APPLICANT: SAGAWA, Hiroaki
; APPLICANT: UEMORI, Takashi
; APPLICANT: YAMAMOTO, Junko
; APPLICANT: TOMONO, Jun
; APPLICANT: KOBAYASHI, Ei-ji
; APPLICANT: ENOKI, Tatsuji
; APPLICANT: TAKEDA, Osamu
; APPLICANT: MIYAKE, Kazuo
; APPLICANT: SATO, Yoshimi
; APPLICANT: MORIYAMA, Mariko
; APPLICANT: SAWARAGI, Haruhisa
; APPLICANT: HAGIYA, Michio
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshi
; TITLE OF INVENTION: A method for amplification of nucleic acids
; FILE REFERENCE: MIYAKI-1
; CURRENT APPLICATION NUMBER: US/09/935,338
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: JP11-076966
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: JP11-370035
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: JP2000-251981
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: JP2000-284419
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: JP2000-288750
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: JP2001-104191
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PCT/JP00/01534
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 233
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Thermotoga maritima
US-09-935-338-233

Query Match      72.3%; Score 34; DB 10; Length 238;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches      5; Conservative      4; Mismatches      0; Indels      0; Gaps      0;

QY      1 GLVPIHQMS 9
DB      176 GLVPIHQMS 184

RESULT 14
US-10-380-430-59
; Sequence 59, Application US/10380430
; Publication No. US20040038366A1
; GENERAL INFORMATION:
; APPLICANT: UEMORI, Takashi
; APPLICANT: SATO, Yoshimi
; APPLICANT: KOYAMA, No. US20040038366A1
; APPLICANT: HIRANO, Ryo
; APPLICANT: TAKAKURA, Hiakaru
; APPLICANT: KOBORI, Hiroshi
; APPLICANT: HASHIMOTO, Yuji
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshi
; TITLE OF INVENTION: THERMOTOLERANT RIBONUCLEASE H
; FILE REFERENCE: UEMORI-1
; CURRENT APPLICATION NUMBER: US/10/380,430
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; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000-280785
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: JP 2001-064074
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/JP01/07930
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 59
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Thermotoga maritima
US-10-380-430-59

Query Match      72.3%; Score 34; DB 15; Length 238;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches      5; Conservative      4; Mismatches      0; Indels      0; Gaps      0;

QY      1 GLVPIHQMS 9
DB      176 GLVPIHQMS 184

RESULT 15
US-10-282-122A-51529
; Sequence 51529, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Olsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.024A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51529
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51529
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Query Match 72.3%; Score 34; DB 15; Length 254;  
 Best Local Similarity 66.7%; Pred. No. 2e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGVPIHQMS 9  
 Db 240 GTTPPIHQMS 248

Search completed: December 15, 2004, 16:54:13  
 Job time : 89.4286 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2004, 16:28:26 ; Search time 10.7143 Seconds  
(without alignments)  
80.822 Million cell updates/sec

Title: US-09-868-605-14\_COPY\_113\_121

Perfect score: 47

Sequence: 1 GLVPIHOMS 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 79:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query % | Match Length | DB ID    | Description        |
|------------|-------|---------|--------------|----------|--------------------|
| 1          | 38    | 80.9    | 330          | 146691   | CD86 precursor - r |
| 2          | 37    | 78.7    | 99           | 2 B83129 | hypothetical prote |
| 3          | 36    | 76.6    | 261          | 2 A11233 | ribonuclease H rnh |
| 4          | 35    | 74.5    | 434          | 2 S5579  | D-nopaline dehydro |
| 5          | 35    | 74.5    | 472          | 2 A13329 | D-nopaline dehydro |
| 6          | 35    | 74.5    | 1493         | 2 AC2555 | hypothetical prote |
| 7          | 34    | 72.3    | 228          | 2 B72320 | ribonuclease H11   |
| 8          | 34    | 72.3    | 254          | 2 B97117 | ribonuclease H11   |
| 9          | 34    | 72.3    | 263          | 2 A81446 | acyl-[acyl-carrier |
| 10         | 34    | 72.3    | 947          | 2 H85088 | hypothetical prote |
| 11         | 34    | 72.3    | 1353         | 2 JC4279 | adenylate cyclase  |
| 12         | 33    | 70.2    | 159          | 2 F83710 | hypothetical prote |
| 13         | 33    | 70.2    | 261          | 2 AG1596 | ribonuclease H rnh |
| 14         | 33    | 70.2    | 278          | 2 F51324 | proteolipid protei |
| 15         | 33    | 70.2    | 405          | 2 B69200 | hypothetical prote |
| 16         | 33    | 70.2    | 407          | 2 E87556 | acyl-CoA dehydroge |
| 17         | 33    | 70.2    | 411          | 2 D75408 | phosphoglycerate k |
| 18         | 33    | 70.2    | 453          | 2 AH0827 | probable prs syste |
| 19         | 33    | 70.2    | 586          | 2 D84710 | hypothetical prote |
| 20         | 33    | 70.2    | 718          | 2 A82352 | iron(III) compound |
| 21         | 33    | 70.2    | 2018         | 2 T34274 | hypothetical prote |
| 22         | 32    | 68.1    | 105          | 2 F84609 | probable cysteine  |
| 23         | 32    | 68.1    | 109          | 2 I40396 | flagellar protein  |
| 24         | 32    | 68.1    | 134          | 2 AE3490 | hiti protein (impo |
| 25         | 32    | 68.1    | 275          | 2 JC7604 | CD86 spliced varia |
| 26         | 32    | 68.1    | 329          | 1 A48754 | B7-2 antigen - hum |
| 27         | 32    | 68.1    | 345          | 2 T12350 | NADH2 dehydrogenas |
| 28         | 32    | 68.1    | 370          | 2 F86236 | protein F14N23.9 l |
| 29         | 32    | 68.1    | 391          | 2 D89926 | 30S ribosomal prot |

|    |    |      |      |          |                    |
|----|----|------|------|----------|--------------------|
| 30 | 32 | 68.1 | 402  | 2 F96640 | hypothetical prote |
| 31 | 32 | 68.1 | 430  | 2 B86805 | hypothetical prote |
| 32 | 32 | 68.1 | 450  | 2 T15154 | hypothetical prote |
| 33 | 32 | 68.1 | 476  | 2 T23213 | hypothetical prote |
| 34 | 32 | 68.1 | 481  | 2 D83466 | probable two-compo |
| 35 | 32 | 68.1 | 622  | 2 T23804 | hypothetical prote |
| 36 | 32 | 68.1 | 653  | 2 T51895 | hypothetical prote |
| 37 | 32 | 68.1 | 741  | 2 US0606 | homeobox protein A |
| 38 | 32 | 68.1 | 747  | 2 AG3031 | conserved hypothet |
| 39 | 32 | 68.1 | 747  | 2 D98254 | hypothetical prote |
| 40 | 32 | 68.1 | 872  | 2 JH0561 | metabotropic gluta |
| 41 | 32 | 68.1 | 978  | 2 H86319 | hypothetical prote |
| 42 | 32 | 68.1 | 1044 | 2 B72338 | galactosyltransfer |
| 43 | 32 | 68.1 | 3600 | 2 D86161 | F1003.12 protein - |
| 44 | 31 | 66.0 | 80   | 2 JT0435 | hypothetical prote |
| 45 | 31 | 66.0 | 80   | 2 T03187 | hypothetical prote |

## ALIGNMENTS

RESULT 1  
146691  
CD86 precursor - rabbit  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 09-Jul-2004  
C/Accession: 146691  
R/Isono, T.; Seto, A.  
Immunogenetics 42, 217-220, 1995  
A/Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecu  
A/Reference number: 146691, MUID:5536849; PMID:7642234  
A/Status: Preliminary; translated from GB/EWBL/DD3J  
A/Molecule type: mRNA  
A/Residues: 1-330 <ISO>  
A/Cross-references: UNIPROT:P42071; GB:D49842; NID:G755098; PIDN:BA08642.1; PID:G75509;  
C/Superfamily: B7-2 antigen

Query Match 80.9%; Score 38; DB 2; Length 330;  
Best Local Similarity 77.8%; Pred. No. 5.4;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9  
DB 119 GLVPIHOMN 127

RESULT 2  
B83129  
hypothetical protein PA4139 (imported) - Pseudomonas aeruginosa (strain PA01)  
C/Species: Pseudomonas aeruginosa  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C/Accession: B83129

R/Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laidig, K.; Lim  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path  
A/Reference number: A82950; MUID:20437337; PMID:10584043

A/Accession: B83129

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-99 <STO>

A/Cross-references: UNIPROT:Q9HWP2; GB:AE004830; GB:AE004091; NID:G950337; PIDN:AA0675;

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA4139

Query Match 78.7%; Score 37; DB 2; Length 99;  
Best Local Similarity 66.7%; Pred. No. 2.3;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9

Db 57 GLVPIHQMS 65

## RESULT 3

ribonuclease H rnh homolog rnhB [imported] - *Listeria monocytogenes* (strain EGD-e)

C/Species: *Listeria monocytogenes*

C/Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004

C/Accession: A11233

R/Glaeser, P.; Frangouli, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecher, D.; Jones, L.M.; Karet, U.

Science 294, 849-852, 2001

A/Authors: Kretz, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maicournam, A.; Ma

ok, C.; Schueller, T.; Simoes, N.; Tixeret, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A/Title: Comparative genomics of *Listeria* species.

A/Reference number: AB1077; MUID:21537279; PMID:11679669

C/Accession: A11233

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-261 <GLA>

A/Cross-references: UNIPROT:O8Y7K4; GB:NC\_003210; PIDN:CAC99351.1; PID:G16410689; GSPDB:

A/Experimental source: strain EGD-e

C/Genetics:

A/Gene: rnhB

C/Superfamily: ribonuclease HII

Query Match

Best Local Similarity 76.6%; Score 36; DB 2; Length 261;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 238 GLVPIHQMS 246

## RESULT 4

D-nopaline dehydrogenase (EC 1.5.1.19) Noxa - *Agrobacterium tumefaciens*

C/Species: *Agrobacterium tumefaciens*

C/Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004

C/Accession: S55579

R/Zanker, H.; Lutz, G.; Langridge, U.; Langridge, P.; Schroeder, J.

submitted to the EMBL Data Library, February 1994

A/Description: Octopine and nopaline oxidases from Ti plasmids of *Agrobacterium tumefaci*

A/Reference number: S55579

C/Accession: S55579

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-434 <ZAN>

A/Cross-references: UNIPROT:Q59158; EMBL:Z30316; NID:G496533; PIDN:CA82963.1; PID:G4965

C/Keywords: oxidoreductase

Query Match

Best Local Similarity 74.5%; Score 35; DB 2; Length 434;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 262 GLVPIHQMS 270

## RESULT 5

D-nopaline dehydrogenase noxa [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont

C/Species: *Agrobacterium tumefaciens*

C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004

C/Accession: A13229

R/Wood, D.W.; Setubal, J.C.; Xaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woc, I

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuliyavin, T.; Levy, R.; Li, M.; McClell

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, B.W.

A/Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A/Reference number: AB2577; MUID:21608550; PMID:11743193

C/Accession: A13229

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-472 <KUR>

A/Cross-references: UNIPROT:O8U699; GB:AE008690; PIDN:AAL46255.1; PID:G17744034; GSPDB:

A/Experimental source: strain C58 (Dupont)

C/Genetics:

A/Gene: noxa

C/Genome: plasmid

Query Match

Best Local Similarity 74.5%; Score 35; DB 2; Length 472;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 262 GLVPIHQMS 270

## RESULT 6

hypothetical protein alr8034 [imported] - *Nostoc* sp. (strain PCC 7120) plasmid pCC7120g

C/Species: *Nostoc* sp. PCC 7120

A/Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C/Accession: AC2555

R/Kaneh, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuch

Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takasawa, M.; Yasuda, M.; Tabata,

DNA Res. 8, 205-213, 2001

A/Title: Complete genomic sequence of the filamentous nitrogen-fixing *Cyanobacterium* An

A/Reference number: AB1807; MUID:21595285; PMID:11759840

C/Accession: AC2555

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1499 <KUR>

A/Cross-references: UNIPROT:O8YK83; GB:AP003603; PIDN:BA877364.1; PID:G17134807; GSPDB:

A/Experimental source: strain PCC 7120

C/Genetics:

A/Gene: alr8034

C/Genome: plasmid

Query Match

Best Local Similarity 74.5%; Score 35; DB 2; Length 1499;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1389 LIPPIHQMS 1396

## RESULT 7

ribonuclease HII - *Thermotoga maritima* (strain MSB8)

C/Species: *Thermotoga maritima*

C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C/Accession: B72320

R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.

Nature 399, 323-329, 1999

A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se

A/Reference number: A72200; MUID:99287316; PMID:10360571

C/Accession: B72320

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-238 <ARN>

A/Cross-references: UNIPROT:O9X017; GB:AE001755; GB:AE000512; NID:G4981432; PIDN:AAD359

A/Experimental source: strain MSB8

C/Genetics:

A:Gene: TW0915  
C:Superfamily: ribonuclease HII  
Query Match 72.3%; Score 34; DB 2; Length 238;  
Best Local Similarity 55.6%; Pred. No. 24;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
DB 176 GVPIHQS 184

RESULT 8  
E97117  
ribonuclease HII [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C>Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: E97117  
R:Rolling, J.; Brelton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: E97117  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-254 <KUR>  
A:Cross-references: UNIPROT:Q97190; GB:AE001437; PIDN:AAK79728.1; PID:g15024732; GSPDB:C  
C:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC1762

Query Match 72.3%; Score 34; DB 2; Length 254;  
Best Local Similarity 66.7%; Pred. No. 26;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
DB 240 GTPPIHQS 248

RESULT 9  
A81446  
acyl-lacyl-carrier-protein [UDP-N-acetylglucosamine O-acyltransferase (EC 2.3.1.129) C]O  
C:Species: Campylobacter jejuni  
C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: A81446  
R:Parhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chilling, C.W.; Quail, M.; Raftery, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel, Nature 403, 665-668, 2000  
A>Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyf  
A:Reference number: A81250; MUID:20150912; PMID:10688204  
A:Accession: A81446  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-263 <PBR>  
A:Cross-references: UNIPROT:Q9PIM1; GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB7274  
A:Experimental source: serotype O2, strain NCTC 11168  
C:Genetics:  
A:Gene: lpxA; Cj0274  
C:Superfamily: acyl-lacyl-carrier-protein [UDP-N-acetylglucosamine O-acyltransferase  
C:Keywords: acyltransferase

Query Match 72.3%; Score 34; DB 2; Length 263;  
Best Local Similarity 85.7%; Pred. No. 27;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
DB 152 GLVPIHQ 158

RESULT 10

H85088  
hypothetical protein AT490830 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: H85088  
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
Nature 402, 769-777, 1999  
A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A:Reference number: A85001; MUID:20083488; PMID:10617198  
A:Accession: H85088  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-947 <STO>  
A:Cross-references: UNIPROT:Q9JDL8; GB:NC\_001268; NID:g7267526; PIDN:CAB78008.1; GSPDB:C  
C:Genetics:  
A:Gene: AT490830  
A:Map position: 4

Query Match 72.3%; Score 34; DB 2; Length 947;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
DB 476 LIPPIHQS 483

RESULT 11  
JC4279  
adenylate cyclase (EC 4.6.1.1) type 10 - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004  
C:Accession: JC4279  
R:Paterson, J.M.; Smith, S.W.; Hartmar, A.U.; Antoni, F.A.  
Biochem. Biophys. Res. Commun. 214, 1000-1008, 1995  
A>Title: Control of a novel adenylyl cyclase by calcineurin.  
A:Reference number: JC4279; MUID:96024597; PMID:7575502  
A:Accession: JC4279  
A:Molecule type: mRNA  
A:Residues: 1-1353 <PAT>  
A:Cross-references: UNIPROT:P51830; EMBL:Z50190  
A:Experimental source: A1T20 cells  
C:Comment: This enzyme is the target of regulation by calcineurin and is a physiological  
messenger molecules.

C:Superfamily: human adenylyl cyclase: guanylate cyclase catalytic domain homology  
C:Keywords: phosphorus-oxygen lyase; transmembrane protein  
F:118-137/Domain: transmembrane #status predicted <TM01>  
F:142-162/Domain: transmembrane #status predicted <TM02>  
F:173-193/Domain: transmembrane #status predicted <TM03>  
F:230-241/Domain: transmembrane #status predicted <TM04>  
F:244-264/Domain: transmembrane #status predicted <TM05>  
F:284-304/Domain: transmembrane #status predicted <TM06>  
F:313-375/Domain: guanylate cyclase catalytic domain homology <GCC>  
F:377-807/Domain: transmembrane #status predicted <TM07>  
F:819-839/Domain: transmembrane #status predicted <TM08>  
F:865-885/Domain: transmembrane #status predicted <TM09>  
F:891-911/Domain: transmembrane #status predicted <TM10>  
F:921-941/Domain: transmembrane #status predicted <TM11>  
F:977-997/Domain: transmembrane #status predicted <TM12>  
F:1031-1246/Domain: guanylate cyclase catalytic domain homology <GCC2>

Query Match 72.3%; Score 34; DB 2; Length 1353;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
DB 1249 GVPIHQHS 1257

RESULT 12  
P83710  
hypothetical protein BH0486 [imported] - Bacillus halodurans (strain C-125)

C/Species: *Bacillus halodurans*  
C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C/Accession: F83710  
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
Molecular Acids Res. 28, 4317-4331, 2000  
A/Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and  
A/Reference number: A83650; MUID:20512582; PMID:11058132  
A/Accession: F83710  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-159 <STO>  
A/Cross-references: UNIPROT:Q9KFCJ; GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BA8042  
C/Genetics:  
A/Supernfamily: *Bacillus subtilis* hypothetical protein ytes  
C/Supernfamily: *Bacillus subtilis* hypothetical protein ytes  
Query Match  
Best Local Similarity 70.2%; Score 33; DB 2; Length 159;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GLVPIHOMS 9  
DB 88 GLVPIHOMS 96  
RESULT 13  
AG1596  
ribonuclease H rnh homolog rnhb [imported] - *Listeria innocua* (strain C1p11262)  
C/Species: *Listeria innocua*  
C/Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C/Accession: AG1596  
R/Glaser, P.; Frangouli, L.; Buchrieser, C.; Amend, A.; Baguer, F.; Berche, P.; Bloeker  
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feint, H.  
D.; Jones, L.M.; Karsch, U.  
Science 294, 849-852, 2001  
A/Authors: Krett, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Macheno, E.; Maltournam, A.; Ma  
ok, C.; Schlueter, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland,  
A/Title: Comparative genomics of *Listeria* species.  
A/Reference number: AB1077; MUID:21537279; PMID:11679669  
A/Accession: AG1596  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-261 <GLA>  
A/Cross-references: UNIPROT:Q92C79; GB:AL592022; PIDN:CAC96543.1; PID:G16413785; GSPDB:G  
A/Experimental source: strain C1p11262  
C/Genetics:  
A/Supernfamily: *ribonuclease H*  
C/Supernfamily: *ribonuclease H*  
Query Match  
Best Local Similarity 70.2%; Score 33; DB 2; Length 261;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GLVPIHOMS 9  
DB 238 GLVPIHOMS 246  
RESULT 14  
151324  
proteolipid protein DW beta - spiny dogfish  
C/Species: *Squalus acanthias* (spiny dogfish)  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C/Accession: 151324  
R/Kitagawa, K.; Sinoway, M.P.; Yang, C.; Gould, R.M.; Colman, D.R.  
Neuron 11, 433-448, 1993  
A/Title: A proteolipid protein gene family: expression in sharks and rays and possible e  
A/Reference number: 151323; MUID:94000610; PMID:838138  
A/Accession: 151324  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-278 <KIT>

A/Cross-references: UNIPROT:P36664; EMBL:U02974; NID:g409971; PIDN:AA059640.1; PID:g409  
C/Supernfamily: myelin proteolipid protein  
Query Match  
Best Local Similarity 70.2%; Score 33; DB 2; Length 278;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GLVPIHQ 7  
DB 181 GLVPIHQ 187  
RESULT 15  
B69200  
hypothetical protein MTH749 - *Methanobacterium thermoautotrophicum* (strain Delta H)  
C/Species: *Methanobacterium thermoautotrophicum*  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: B69200  
R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
; Ott, D.; Spadefora, R.; Vitatore, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.  
K.; S.; Church, G.M.; Daniele, C.O.; Rao, U.; Rice, P.; Noelling, J.; Reeve, J.N.  
U. Bacteriol. 179, 7135-7155, 1997  
A/Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: funct  
A/Reference number: A69000; MUID:98037514; PMID:9371463  
A/Accession: B69200  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-405 <MTH>  
A/Cross-references: UNIPROT:Q26844; GB:AE000853; GB:AE000666; NID:g2621824; PIDN:AA852525  
A/Experimental source: strain Delta H  
C/Genetics:  
A/Supernfamily: *MTH749*  
Query Match  
Best Local Similarity 70.2%; Score 33; DB 2; Length 405;  
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GLVPIHOMS 9  
DB 69 GMPPIHOMS 77

Search completed: December 15, 2004, 16:38:00  
Job time: 13.7143 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comphen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2004, 16:24:31, Search time 49.7143 Seconds  
(without alignments)  
104.163 Million cell updates/sec

Title: US-09-868-605-14\_COPY\_113\_121

Perfect score: 47

Sequence: 1 GLVPIHOMS 9

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 47    | 100.0       | 325    | 2     | C02838      |
| 2          | 44    | 93.6        | 329    | 2     | Q9XSX6      |
| 3          | 44    | 93.6        | 332    | 2     | Q9GM27      |
| 4          | 44    | 93.6        | 332    | 2     | Q9SL16      |
| 5          | 41    | 87.2        | 329    | 2     | Q9TTF2      |
| 6          | 41    | 87.2        | 329    | 2     | Q9TTF2      |
| 7          | 39    | 83.0        | 330    | 2     | Q9GLJ3      |
| 8          | 38    | 80.9        | 330    | 1     | CD86_RABBIT |
| 9          | 38    | 80.9        | 412    | 2     | Q89E49      |
| 10         | 37    | 78.7        | 378    | 2     | Q8HWP2      |
| 11         | 37    | 78.7        | 378    | 2     | Q7MD30      |
| 12         | 37    | 78.7        | 378    | 2     | Q8D611      |
| 13         | 37    | 78.7        | 812    | 2     | Q7UFI1      |
| 14         | 36    | 76.6        | 90     | 2     | Q84DX1      |
| 15         | 36    | 76.6        | 126    | 2     | Q89Y03      |
| 16         | 36    | 76.6        | 251    | 2     | Q881X8      |
| 17         | 36    | 76.6        | 261    | 1     | RNH2_LISMO  |
| 18         | 36    | 76.6        | 411    | 2     | Q6NL37      |
| 19         | 36    | 76.6        | 411    | 2     | Q810H8      |
| 20         | 36    | 76.6        | 411    | 2     | AAS93776    |
| 21         | 36    | 76.6        | 1081   | 2     | Q7UHS5      |
| 22         | 36    | 76.6        | 6858   | 2     | Q7QUM1      |
| 23         | 35    | 74.5        | 257    | 1     | LPXA_FUSNN  |
| 24         | 35    | 74.5        | 257    | 1     | Q7P452      |
| 25         | 35    | 74.5        | 314    | 2     | Q7X9W7      |
| 26         | 35    | 74.5        | 425    | 1     | Y4RF_RHISN  |
| 27         | 35    | 74.5        | 434    | 2     | Q59158      |
| 28         | 35    | 74.5        | 472    | 2     | Q7D208      |
| 29         | 35    | 74.5        | 472    | 2     | Q9R691      |
| 30         | 35    | 74.5        | 472    | 2     | Q8U699      |
| 31         | 35    | 74.5        | 1323   | 2     | Q8SV50      |

## ALIGNMENTS

|    |    |      |      |   |             |                     |
|----|----|------|------|---|-------------|---------------------|
| 32 | 35 | 74.5 | 1334 | 1 | CYA9_CHICK  | Q9d9g6 gallus gall  |
| 33 | 35 | 74.5 | 1499 | 2 | Q8YK63      | Q8YK63 anabaena sp  |
| 34 | 34 | 72.3 | 226  | 2 | Q7NNLB      | Q7nnl8 gloebacter   |
| 35 | 34 | 72.3 | 238  | 1 | RNH2_THEMA  | Q9X017 thermotoga   |
| 36 | 34 | 72.3 | 249  | 1 | ABG1_LACTIC | Q48725 lactococcus  |
| 37 | 34 | 72.3 | 250  | 2 | Q8DSH5      | Q8dsh5 streptococc  |
| 38 | 34 | 72.3 | 254  | 1 | RNH2_CIOAB  | Q97190 clostridium  |
| 39 | 34 | 72.3 | 263  | 1 | LPXA_CAMJF  | Q9p1n1 campylobact  |
| 40 | 34 | 72.3 | 281  | 2 | P94301      | P94301 bacillus fi  |
| 41 | 34 | 72.3 | 315  | 2 | Q82CR7      | Q82cr7 streptomyce  |
| 42 | 34 | 72.3 | 400  | 2 | Q6M5E1      | Q6m5e1 corynebacte  |
| 43 | 34 | 72.3 | 400  | 2 | CAF21448    | Ca121448 corynebac  |
| 44 | 34 | 72.3 | 479  | 2 | Q72D66      | Q72d66 desulfocvibr |
| 45 | 34 | 72.3 | 479  | 2 | AAS95543    | Aas95543 desulfocvi |

## RESULT 1

|    |                                                                       |                                         |      |         |
|----|-----------------------------------------------------------------------|-----------------------------------------|------|---------|
| ID | C02838                                                                | PRELIMINARY;                            | PRT; | 325 AA. |
| AC | Q02838;                                                               |                                         |      |         |
| DT | 01-JUL-1997                                                           | (TRENBLrel. 04, Created)                |      |         |
| DT | 01-JUL-1997                                                           | (TRENBLrel. 04, Last sequence update)   |      |         |
| DT | 01-OCT-2003                                                           | (TRENBLrel. 25, Last annotation update) |      |         |
| DE | B7-2.                                                                 |                                         |      |         |
| GN | Name=CD86;                                                            |                                         |      |         |
| OS | Sus scrofa (pig).                                                     |                                         |      |         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |                                         |      |         |
| OC | Mammalia; Eutheria; Cetartiodactyla; Suiua; Suidae; Sus.              |                                         |      |         |
| OX | NCBI_TaxID=9823;                                                      |                                         |      |         |
| RN | [1]                                                                   |                                         |      |         |
| RP | SEQUENCE FROM N.A.                                                    |                                         |      |         |
| RX | MEDLINE=97047772; PubMed=8892613;                                     |                                         |      |         |
| RA | Maher S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,              |                                         |      |         |
| RA | Bothwell A.L.;                                                        |                                         |      |         |
| RT | "Porcine endothelial CD86 is a major costimulator of xenogeneic human |                                         |      |         |
| RT | T cells: cloning, sequencing, and functional expression in human      |                                         |      |         |
| RT | endothelial cells."                                                   |                                         |      |         |
| RL | J. Immunol. 157:3838-3844(1996).                                      |                                         |      |         |
| DR | EMBL; L76099; AAB61307.1; -.                                          |                                         |      |         |
| DR | HSSP; P42081; INCN.                                                   |                                         |      |         |
| DR | InterPro; IPR007110; IG-1like.                                        |                                         |      |         |
| DR | InterPro; IPR003596; IG_v.                                            |                                         |      |         |
| DR | Pfam; PF00047; IG_1.                                                  |                                         |      |         |
| DR | SMART; SMO0406; IGV; 1.                                               |                                         |      |         |
| DR | PROSITE; PS00835; IG_LIKE; 1.                                         |                                         |      |         |
| DR | SEQUENCE 325 AA; 36527 MW; 988BB08137B0597D CRC64;                    |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9                                                         |                                         |      |         |
| Db | 113 GLVPIHOMS 121                                                     |                                         |      |         |
| QY |                                                                       |                                         |      |         |
| Db |                                                                       |                                         |      |         |
| QY | 100.0%; Score 47; DB 2; Length 325;                                   |                                         |      |         |
| Db | Best Local Similarity 100.0%; Pred. No. 0.53;                         |                                         |      |         |
| QY | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;            |                                         |      |         |
| QY | 1 GLVPIHOMS 9</                                                       |                                         |      |         |

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RP SEQUENCE FROM N.A.
RX MEDLINE=20180222; PubMed=10713336;
RA Choi I.S., Hash S.M., Winslow B.J., Collisson E.W.;
RT "Sequence analyses of feline B7 costimulatory molecules.";
RL Vet. Immunol. Immunopathol. 73:219-231(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Choi I.S., Hash S., Winslow B.J., Collisson E.W.;
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF157827; AAD42974.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 329 AA; 37481 MW; A10621E3C00A08B8 CRC64;

Query Match
Best Local Similarity 93.6%; Score 44; DB 2; Length 329;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9
DB 120 GLVPIHOMS 128

RESULT 3
O9GMZ7 PRELIMINARY; PRT; 332 AA.
ID O9GMZ7
AC O9GMZ7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE B-lymphocyte activation antigen B7-2 (CD86).
GN Name=CD86;
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX NCBI_TaxId=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20485322; PubMed=11029611;
RA Nishimura Y., Shimojima M., Miyazawa T., Sato E., Nakamura K.,
RA Izumiya Y., Ikeda Y., Mikami T., Takahashi E.;
RT "Molecular cloning of the CDNA encoding the feline B-lymphocyte
RT activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which
RT interact with human CTLA4-Ig.";
RL Eur. J. Immunogenet. 27:427-430(2000).
DR EMBL; AB030652; BAB11688.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 332 AA; 37812 MW; 672C8B3667D1E3C0 CRC64;

Query Match
Best Local Similarity 93.6%; Score 44; DB 2; Length 332;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9
DB 120 GLVPIHOMS 128

RESULT 4
O9SL16 PRELIMINARY; PRT; 332 AA.
ID O9SL16
AC O9SL16;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CD8c.

```

```

GN Name=CD86;
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX NCBI_TaxId=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21390213; PubMed=11498243;
RA Yang S., Sellins K.S., Powell T., Storeman E., Sim G.K.;
RT "Novel transcripts encoding secreted forms of feline CD80 and CD86
RT costimulatory molecules.";
RL Vet. Immunol. Immunopathol. 81:15-21(2001).
DR EMBL; AY007704; AAG23342.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 332 AA; 37826 MW; 8BFC8B3667D1E3D8 CRC64;

Query Match
Best Local Similarity 93.6%; Score 44; DB 2; Length 332;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9
DB 120 GLVPIHOMS 128

RESULT 5
O9TF1 PRELIMINARY; PRT; 280 AA.
ID O9TF1
AC O9TF1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TREMBLrel. 26, Last annotation update)
DE Truncated B7-2 protein.
GN Name=CD86;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20093986; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New forms of dog CD80 and CD86 transcripts that encode secreted B7
RT molecules.";
RL Immunogenetics 50:349-353(1999).
DR EMBL; AF106827; AAF17298.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 280 AA; 32255 MW; 3C8EBCA4D826A7F3 CRC64;

Query Match
Best Local Similarity 87.2%; Score 41; DB 2; Length 280;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9
DB 119 GLVPIHOMS 127

RESULT 6
O9TF2 PRELIMINARY; PRT; 329 AA.
ID O9TF2
AC O9TF2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)

```



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DT 01-MAY-2000 (TEMBLrel. 13, last sequence update)
DE B7-2 protein.
DB 01-MAR-2004 (TEMBLrel. 26, last annotation update)
OS Name=CD86;
GN Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2009396; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New forms of dog CD80 and CD86 transcripts that encode secreted B7
  molecules."
RL Immunogenetics 50:349-353(1999).
DR EMBL; AF106826; AAF17297.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 329 AA; 37774 MW; D98B63437BF7B73 CRC64;

Query Match      87.2%; Score 41; DB 2; Length 329;
Best Local Similarity 77.8%; Pred. No. 8.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPHIOMS 9
Db 119 GLVPHIQMN 127

RESULT 7
Q9GLJ3 PRELIMINARY; PRT; 284 AA.
AC Q9GLJ3;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE C86 antigen (Fragment).
GN Name=CD86;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Peripheral blood;
RA Brooke G.P., Howard C.J., Parsons K.R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL291475; CAC13140.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON TER 284
SQ SEQUENCE 284 AA; 32021 MW; 797BB639E297841 CRC64;

Query Match      83.0%; Score 39; DB 2; Length 284;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPHIOMS 9
Db 126 GLVSIHOMS 134

RESULT 8
CD86_RABBIT

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ID CD86_RABBIT STANDARD; PRT; 330 AA.
AC P42071;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE B lymphocyte activation antigen CD86 precursor (Activation B7-2
  antigen)
GN Name=CD86;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=B/7 X CHB; HM;
RX MEDLINE=95369849; PubMed=7642234;
RA Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
  costimulatory molecules."
RL Immunogenetics 42:217-220(1995).
CC -!- FUNCTION: Receptor involved in the costimulatory signal essential
  for T lymphocyte proliferation and interleukin 2 production, by
  binding CD28 or CTLA-4. May play a critical role in the early
  events of T cell activation and costimulation of naive T cells,
  such as deciding between immunity and anergy that is made by T
  cells within 24 hours after activation.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; D49842; BA08642.1; -.
DR PIR; I46591; I46591.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; T-cell;
  Transmembrane.
FT SIGNAL 1..22
FT CHAIN 23..330
FT DOMAIN 23..247
FT TRANSMEM 248..268
FT DOMAIN 269..330
FT DOMAIN 33..127
FT DOMAIN 150..225
FT DISULFID 40..110
FT DISULFID 157..218
FT CARBOHYD 33..33
FT CARBOHYD 135..135
FT CARBOHYD 146..146
FT CARBOHYD 154..154
FT CARBOHYD 177..177
FT CARBOHYD 192..192
FT CARBOHYD 198..198
FT CARBOHYD 213..213
SQ SEQUENCE 330 AA; 37142 MW; 935CD65C57B3EB1 CRC64;

Query Match      80.9%; Score 38; DB 1; Length 330;
Best Local Similarity 77.8%; Pred. No. 36;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPHIOMS 9

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Db 119 GLVPIXOM 127

## RESULT 9

089E49 PRELIMINARY; PRT; 412 AA.  
AC 089E49;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE B1r7238 protein.  
GN OrderedlocusNames=B1r7238;  
OS Bradyrhizobium japonicum.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae; Bradyrhizobiaceae;  
OC NCBI\_TaxId=375;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=USDA110;  
RX MEDLINE=22484998; PubMed=12597275;  
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,  
RA Kasehara M., Matsumoto M., Shimizu S., Tsuruoka H., Wada T., Yamada M.,  
RA Tabata S.;  
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
Bradyrhizobium japonicum USDA110.";  
RL DNA Res. 9:189-197(2002).  
DR EMBL; AP005961; BAC52503.1; -  
KW Complete proteome.  
SQ SEQUENCE 412 AA; 43969 MW; B801F68936C8F7BE CRC64;

Query Match 80.9%; Score 38; DB 2; Length 412;  
Best Local Similarity 66.7%; Pred. No. 45;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLVPIXOMS 9  
Db 276 GLVPIXOMS 284

## RESULT 10

09HWP2 PRELIMINARY; PRT; 99 AA.  
AC 09HWP2;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Hypothetical protein.  
GN OrderedlocusNames=PA4139;  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OC NCBI\_TaxId=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 15692 / PA01;  
RX MEDLINE=20437337; PubMed=10984043;  
RA Hickey M.T., Brinkman F.S.D., Hutnagle W.O., Kowalik D.V., Lagrou M.,  
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Webman S., Yuan Y.,  
RA Brody L.L., Coulter S.N., Folger K.R., West A., Labig K., Lim R.M.,  
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
RA Reiter J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;  
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
opportunistic pathogen.";  
RL Nature 406:959-964(2000).  
DR EMBL; AE004830; AAC07526.1; -  
DR PIR; B83129; B83129.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 99 AA; 10437 MW; 62706B205A63F966 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 99;

Best Local Similarity 66.7%; Pred. No. 17;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLVPIXOMS 9  
Db 57 GLVPIXOMS 65

## RESULT 11

07MD30 PRELIMINARY; PRT; 378 AA.  
AC 07MD30;  
DT 01-MAR-2004 (TREMBLrel. 26, Created)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE N-acetylglucosamine-6-phosphate deacetylase.  
GN Name=VVA1206;  
OS Vibrio vulnificus (strain V016).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrrio.  
OC NCBI\_TaxId=196600;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=14656965;  
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,  
RA Liao T.-L., Liu Y.-M., Chen H.-Y., Shen A.B.-T., Li J.-C., Su T.-L.,  
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;  
RT "Comparative genome analysis of Vibrio vulnificus, a marine  
pathogen.";  
RL Genome Res. 13:2577-2587(2003).  
DR EMBL; AP005349; BAC97232.1; -  
DR GO; GO:0016787; Phosphatase activity; IEA.  
DR GO; GO:0008448; N-acetylglucosamine-6-phosphate deacetylase; IEA.  
DR GO; GO:0006044; N-acetylglucosamine metabolism; IEA.  
DR InterPro; IPR006680; Amidohydrolyase.  
DR InterPro; IPR011550; Amidohydrolyase.  
DR InterPro; IPR003764; Naga.  
DR Pfam; PF01979; Amidohydrolyase.  
DR ProDom; PD001248; Amidohydrolyase.  
DR TIGRfam; TIGR00221; naga; 1.  
SQ SEQUENCE 378 AA; 41513 MW; C8B55701F5C2F5BD CRC64;

Query Match 78.7%; Score 37; DB 2; Length 378;  
Best Local Similarity 77.8%; Pred. No. 66;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLVPIXOMS 9  
Db 32 GLVPIXOMS 40

## RESULT 12

08D611 PRELIMINARY; PRT; 378 AA.  
AC 08D611;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE N-acetylglucosamine-6-phosphate deacetylase.  
GN OrderedlocusNames=VY20736;  
OS Vibrio vulnificus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrrio.  
OC NCBI\_TaxId=672;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CMP6;  
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.T., Moon Y.H., Jeong H.,  
RA Choe H.E.;  
RT "Complete genome sequence of Vibrio vulnificus CMP6.";  
RL Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF016810; AAC07668.1; -  
DR GO; GO:0016787; Phosphatase activity; IEA.

DR GO: GO:0008448; F:N-acetylglucosamine-6-phosphate deacetylase. . .; IEA.  
 DR GO: GO:0006044; F:N-acetylglucosamine metabolism; IEA.  
 DR InterPro: IPR006680; Amidohydro\_1.  
 DR InterPro: IPR011550; Amidohydro\_1.  
 DR InterPro: IPR011059; Metallo\_hydrolase.  
 DR InterPro: IPR003764; Naga\_hydrolyase.  
 DR Pfam: PF01979; Amidohydro\_1; 1.  
 DR ProDom: PD001248; Amidohydro\_1; 1.  
 DR TrRfam: TRFR00221; naga; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 378 AA; 41494 MW; 5084CDA042824B68 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 378;  
 Best Local Similarity 77.8%; Pred. No. 66;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9  
 DB 32 GLVPIHOMS 40

## RESULT 13

Q7UIF1 PRELIMINARY; PRT; 812 AA.  
 AC Q7UIF1;  
 DT 01-OCT-2003 (TRENBLREL. 25, Created)  
 DT 01-OCT-2003 (TRENBLREL. 25, Last sequence update)  
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)  
 DE Serine/threonine-protein kinase.  
 GN OrderedLocustNames=RB12572;  
 OS Rhodospirillum rubrum.  
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
 OC Planctomycetaceae; Pirellula.  
 OX NCBI\_TaxID=117;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1;  
 RX MEDLINE=22735913; PubMed=12835416;  
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,  
 RA Ludwig W., Gade D., Beck K., Borzym K., Heilmann K., Rabus R.,  
 RA Schleuter H., Aumann R., Reinhardt R.;  
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.  
 strain 1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL: BX294155; CAD77663.1; -  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO: GO:0016740; F:transferase activity; IEA.  
 DR GO: GO:0006468; F:protein amino acid phosphorylation; IEA.  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR ProSite: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Complete proteome; Kinase;  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 812 AA; 90937 MW; C812980D435HEAA CRC64;

Query Match 78.7%; Score 37; DB 2; Length 812;  
 Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOM 8  
 DB 138 GLVPIHOM 145

RESULT 14  
 Q84DX1 PRELIMINARY; PRT; 90 AA.

AC Q84DX1;  
 DT 01-JUN-2003 (TRENBLREL. 24, Created)  
 DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)  
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
 DE Possible VUV repeat protein.  
 OS Tropheryma whipplei (Whipple's bacillus) (Tropheryma whippelii).  
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;  
 OC Micrococciaceae; Cellulomonadaceae; Tropheryma.  
 OX NCBI\_TaxID=2039;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22632143; PubMed=12747404;  
 RA Matwald M., Lepp P.W., Reiman D.A.;  
 RT "Analysis of conserved non-rRNA genes of Tropheryma whippelii.";  
 RL Syst. Appl. Microbiol. 26:3-12(2003).  
 DR EMBL: AF483650; AA084489.1;  
 SQ SEQUENCE 90 AA; 9885 MW; C1DC13F5A46B471 CRC64;

Query Match 76.6%; Score 36; DB 2; Length 90;  
 Best Local Similarity 87.5%; Pred. No. 25;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LVPIHOMS 9  
 DB 25 LVPIHOMS 32

## RESULT 15

Q89Y03 PRELIMINARY; PRT; 126 AA.  
 AC Q89Y03;  
 DT 01-JUN-2003 (TRENBLREL. 24, Created)  
 DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)  
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
 DE Cytochrome O ubiquinol oxidase subunit IV.  
 GN Name=Cyod; OrderedLocustNames=dlr0152;  
 OS Bradyrhizobium japonicum.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae; Bradyrhizobium.  
 OX NCBI\_TaxID=375;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USDA110;  
 RX MEDLINE=22484998; PubMed=12597275;  
 RA Karako T., Nakamura Y., Sato S., Minamisawa K., Uehimi T.,  
 RA Sasamoto S., Watanabe A., Idegawa K., Iiguchi M., Kawashima K.,  
 RA Kohara M., Matsunoto M., Shimo S., Tsunoka H., Wada T., Yamada M.,  
 RA Tabata S.;  
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
 Bradyrhizobium japonicum USDA110.";  
 RL DNA Res. 9:188-197(2002).  
 DR EMBL: AP005935; BAC45417.1; -  
 DR InterPro: IPR005171; COX4\_pro.  
 DR Pfam: PF03626; COX4\_pro; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 126 AA; 13951 MW; 919D87A5633BP1B3 CRC64;

Query Match 76.6%; Score 36; DB 2; Length 126;  
 Best Local Similarity 75.0%; Pred. No. 35;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVPIHOMS 9  
 DB 116 LVPIHOMS 123

Search completed: December 15, 2004, 16:33:36  
 Job time : 51.7143 secs

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OM protein - protein search, using sw model

```
Run on:      December 15, 2004, 16:27:41 ; Search time 129.143 Seconds
              (without alignments)
              33.333 Million cell updates/sec
```

```
Title: US-09-868-605-14_COPY_151_162
Perfect score: 69
Sequence: 1 CSSTGYPEPQR 12
```

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
```

```
Database :
1: Geneseqp23Sep04:*
2: Geneseqp1980s:*
3: Geneseqp1990s:*
4: Geneseqp2000s:*
5: Geneseqp2001s:*
6: Geneseqp2002s:*
7: Geneseqp2003as:*
8: Geneseqp2003bs:*
9: Geneseqp2004as:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID       | Description         |
|------------|-------|-------------|--------|----|----------|---------------------|
| 1          | 69    | 100.0       | 29     | 3  | AAV95330 | AAV95330 OVA323-330 |
| 2          | 69    | 100.0       | 250    | 2  | AAW14944 | AAW14944 Chimeric   |
| 3          | 69    | 100.0       | 325    | 3  | AAV95321 | AAV95321 P19 coat   |
| 4          | 69    | 100.0       | 325    | 3  | AAV95324 | AAV95324 Human coat |
| 5          | 54    | 78.3        | 280    | 2  | AAV41078 | AAV41078 Canine B   |
| 6          | 54    | 78.3        | 329    | 2  | AAV41076 | AAV41076 Canine B   |
| 7          | 54    | 78.3        | 329    | 3  | AAV32278 | AAV32278 Cat CP86   |
| 8          | 54    | 78.3        | 329    | 3  | AAV32285 | AAV32285 Feline CT  |
| 9          | 54    | 78.3        | 329    | 3  | AAV17734 | AAV17734 Feline CT  |
| 10         | 54    | 78.3        | 329    | 5  | AAU78121 | AAU78121 Feline CT  |
| 11         | 54    | 78.3        | 332    | 2  | AAV41079 | AAV41079 Feline B7  |
| 12         | 51    | 73.9        | 102    | 3  | AAW08473 | AAW08473 Human B 1  |
| 13         | 51    | 73.9        | 102    | 3  | AAW37093 | AAW37093 Human B7   |
| 14         | 51    | 73.9        | 244    | 2  | AAW90209 | AAW90209 hb7, 1h15  |
| 15         | 51    | 73.9        | 246    | 2  | AAW68005 | AAW68005 Human B7   |
| 16         | 51    | 73.9        | 246    | 4  | AAW83837 | AAW83837 Amino acid |
| 17         | 51    | 73.9        | 260    | 2  | AAW42339 | AAW42339 CD86 extr  |
| 18         | 51    | 73.9        | 323    | 2  | AAW71478 | AAW71478 B70 type   |
| 19         | 51    | 73.9        | 323    | 3  | AAV44490 | AAV44490 Human B7   |
| 20         | 51    | 73.9        | 323    | 5  | AAE15830 | AAE15830 Human co   |
| 21         | 51    | 73.9        | 323    | 8  | ADD25560 | ADD25560 Binding c  |
| 22         | 51    | 73.9        | 323    | 7  | ADJ54625 | ADJ54625 Human B7   |
| 23         | 51    | 73.9        | 324    | 5  | AAO15801 | AAO15801 Human B7   |
| 24         | 51    | 73.9        | 329    | 2  | AAW67984 | AAW67984 Human B 1  |
| 25         | 51    | 73.9        | 329    | 2  | AAW08467 | AAW08467 Human B 1  |

[illegible]





XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)  
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be  
 CC expressed by standard recombinant methodology. The nucleic acid molecules  
 CC and the encoded proteins can be used for preventing or treating diseases,  
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor  
 CC development, graft rejection, inflammation, arthritic and atopic diseases  
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,  
 CC cats, cattle, sheep or pets. The products can also be used for detection,  
 CC diagnosis and drug screening  
 XX  
 SQ Sequence 280 AA;  
 Query Match 78.3%; Score 54; DB 2; Length 280;  
 Best Local Similarity 81.8%; Pred. No. 2.2;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CSSTGYPEPQ 11  
 DB 158 CSSTGYPEPK 168  
 RESULT 6  
 AAY41076  
 ID AAY41076 standard; protein; 329 AA.  
 XX  
 AC AAY41076;  
 XX  
 DT 20-DEC-1999 (first entry)  
 XX  
 DE Canine B7-2 protein.  
 XX  
 KM B7/ CTLA4: T cell costimulatory protein; dog; cat; autoimmune disease;  
 KM allergic reaction; infectious diseases; tumor development; canine;  
 KM graft rejection; inflammation; arthritis; atopic dermatitis.  
 XX  
 OS Canis familiaris.  
 XX  
 PN MO3947558-A2.  
 XX  
 PD 23-SEP-1999.  
 XX  
 PF 19-MAR-1999; 99WO-US006187.  
 XX  
 PR 19-MAR-1998; 98US-0078765P.  
 PR 17-APR-1998; 98US-00062597.  
 XX  
 PA (HESK-) HESKA CORP.  
 XX  
 PI Sim G, Yang S, Sellins KS;  
 DR WPI, 1999-571822/48.  
 DR N-PSDB; AA27913, AA27915.  
 XX  
 PT New isolated B7 and CTLA4 nucleic acids, used to develop products for  
 PT treating, e.g. autoimmune and atopic diseases.  
 XX  
 PS Claim 4; Page 97-99; 148pp; English.  
 XX  
 CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)  
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be  
 CC expressed by standard recombinant methodology. The nucleic acid molecules  
 CC and the encoded proteins can be used for preventing or treating diseases,  
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor  
 CC development, graft rejection, inflammation, arthritic and atopic diseases  
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,  
 CC cats, cattle, sheep or pets. The products can also be used for detection,  
 CC diagnosis and drug screening  
 XX  
 SQ Sequence 329 AA;  
 Query Match 78.3%; Score 54; DB 2; Length 329;  
 Best Local Similarity 81.8%; Pred. No. 2.6;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CSSTGYPEPQ 11  
 DB 158 CSSTGYPEPK 168  
 RESULT 7  
 AAY32278  
 ID AAY32278 standard; protein; 329 AA.  
 XX  
 AC AAY32278;  
 XX  
 DT 12-SEP-2003 (revised)  
 DT 15-FEB-2000 (first entry)  
 XX  
 DE Cat CD86 (B7-2) ligand.  
 XX  
 KM CD86; B7-2; ligand; cat; vaccine; feline immunodeficiency virus; FIV;  
 KM feline leukaemia virus; feline infectious peritonitis virus;  
 KM feline parvovirus; feline coronavirus; feline calicivirus; feline reovirus-3;  
 KM feline rotavirus; feline coronavirus; feline syncytial virus;  
 KM feline sarcoma virus; feline herpesvirus; feline Borna disease;  
 KM rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;  
 KM parasite; autoimmune disease; transplant rejection; therapy.  
 XX  
 OS Felis catus.  
 XX  
 PN WO9557271-A2.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 30-APR-1999; 99WO-US009502.  
 XX  
 PR 01-MAY-1998; 98US-00071699.  
 XX  
 PA (TEXA) TEXAS A & M SYSTEM.  
 XX  
 PI Collison EW, Hash SM, Choi I;  
 DR WPI, 2000-052972/04.  
 DR N-PSDB; AA234785.  
 XX  
 PT Novel feline proteins used to produce feline vaccines which prevent  
 PT infectious disease or to promote growth in homologous or heterologous  
 PT species.  
 XX  
 PS Example 1A; Fig 3A; 186pp; English.  
 XX  
 CC The present sequence represents feline CD86 (B7-2) ligand, as predicted  
 CC from isolated cDNA of peripheral blood mononuclear cells. The  
 CC coexpression of CD86 with the costimulatory molecules CD28 (see AAY32279)  
 CC and a tumour antigen or an antigen from a pathogenic organism has the  
 CC ability to activate or enhance activation of T-lymphocytes. Coexpression  
 CC of CD86 with CTLA-4 (see AAY32280) has the ability to regulate activation  
 CC of T-lymphocytes. The invention provides isolated nucleic acids encoding  
 CC feline CD86 ligand, feline CD80 (B7-1) ligand, feline CD28 receptor or  
 CC feline CTLA-4 (CD152) receptor, as well as vectors comprising the nucleic  
 CC acids, and polypeptides encoded by the nucleic acids. It also provides  
 CC vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and  
 CC further comprising immunogens derived from pathogens, especially feline  
 CC immunodeficiency virus (FIV), feline leukaemia virus, feline infectious  
 CC peritonitis virus, feline parvovirus, feline coronavirus, feline calicivirus,  
 CC feline reovirus-3, feline rotavirus, feline coronavirus, feline syncytial  
 CC virus, feline sarcoma virus, feline herpesvirus, feline Borna disease  
 CC virus, rabies virus, chlamydia, Toxoplasmosis gondii, Dirofilaria  
 CC immitis, or a flea, bacterial pathogen, or parasite (all claimed).  
 CC Vaccines capable of enhancing an immune response, and vaccines capable of  
 CC suppressing an immune response (suitable for treating an autoimmune  
 CC disease or tissue or organ transplant rejection) are claimed. (Updated on  
 CC 12-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 329 AA;



Query Match 78.3%; Score 54; DB 3; Length 329;  
 Best Local Similarity 81.8%; Pred. No. 2.6;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11  
 DB 159 CSSTQGYPEPK 169

RESULT 8  
 ID AAY32285 standard; protein; 329 AA.

XX AAY32285;

DT 12-SEP-2003 (revised)

DT 28-FEB-2000 (first entry)

XX Feline CD86 (B7-2).

XX CD86; B7-2; feline; cat; recombinant virus; vaccine; immunomodulator;

XX tumour; cancer; therapy.

XX Felis catus.

XX WO957295-A1.

XX 11-NOV-1999.

XX 30-APR-1999; 99WO-US009504.

XX 01-MAY-1998; 98US-00071711.

XX (SCHE ) SCHERING-PLOUGH LTD.

XX (SCHE ) SCHERING-PLOUGH VETERINARY CORP.

XX Winslow BJ, Cochran MD;

XX WPI: 2000-062155/05.

XX N-PSDB; AA234838.

XX Novel recombinant virus useful as immunomodulators, particularly in

XX vaccines.

XX Disclosure; Fig 3A; 230pp; English.

CC This sequence represents feline CD86 (B7-2), as deduced from peripheral  
 CC blood mononuclear cell cDNA (see AA234838). Manipulating the expression  
 CC of CD28 or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)  
 CC regulates T cell proliferation and cytokine release. The invention  
 CC relates to a recombinant virus that contains at least one foreign nucleic  
 CC acid, inserted into a nonessential genomic region, that encodes feline  
 CC CD86, CD80, CD86 or CTLA-4 protein, or their immunogenic fragments, and  
 CC is expressed when the recombinant virus is introduced into a suitable  
 CC host. The invention also provides a recombinant virus further comprising  
 CC a foreign nucleic acid encoding an immunogen derived from a feline  
 CC pathogen; recombinant viruses capable of enhancing an immune response to  
 CC protect against disease; recombinant viruses expressing antitumor  
 CC sequences, capable of suppressing an immune response in a feline, e.g.,  
 CC for treatment of autoimmune disease or transplant rejection; and  
 CC recombinant viruses expressing DNA encoding CD80 and/or CD86 used to  
 CC reduce or eliminate a tumour in cats. (Updated on 12-SEP-2003 to  
 CC standardise OS field)

XX Sequence 329 AA;

Query Match 78.3%; Score 54; DB 3; Length 329;  
 Best Local Similarity 81.8%; Pred. No. 2.6;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11  
 DB 159 CSSTQGYPEPK 169

DB 159 CSSTQGYPEPK 169

RESULT 9  
 ID AA017734 standard; protein; 329 AA.

XX AA017734;

XX 08-AUG-2002 (first entry)

XX Feline CD86.

XX Cat; CD28; CTLA-4; CD86; immunogen; vaccine; viral infection;

XX feline immunodeficiency disease; feline infectious peritonitis;

XX feline leukaemia virus; cancer; degenerative disease; autoimmune disease;

XX virucide; immunomodulator; cytostatic; immunodeficiency.

XX Felis catus.

XX US2002051792-A1.

XX 02-MAY-2002.

XX 30-APR-1999; 99US-00303040.

XX 01-MAY-1998; 98US-0083870P.

XX (WINSLOW B J.

XX (COCHRAN M D.

XX Winslow BJ, Cochran MD;

XX WPI: 2002-415200/44.

XX N-PSDB; AAL46840.

XX New recombinant virus, useful for immunizing felines to prevent or treat

XX feline immunodeficiency virus, comprises foreign nucleic acid encoding

XX feline cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or

XX CTLA-4.

XX Disclosure; Fig 3; 77pp; English.

CC The present invention relates to a recombinant virus comprising at least  
 CC one foreign nucleic acid encoding a protein selected from feline  
 CC cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or CTLA-4,  
 CC which is capable of expression when the virus is introduced into an  
 CC appropriate host. The virus can be administered to the feline in order to  
 CC elicit or enhance an immune response to prevent or treat feline  
 CC immunodeficiency disease, feline leukemia, feline infectious peritonitis,  
 CC cancer, degenerative and autoimmune diseases and immunodeficiency. The  
 CC present sequence is a cytotoxic T lymphocyte accessory molecule described  
 CC in the exemplification of the invention

XX Sequence 329 AA;

Query Match 78.3%; Score 54; DB 5; Length 329;  
 Best Local Similarity 81.8%; Pred. No. 2.6;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11  
 DB 159 CSSTQGYPEPK 169

RESULT 10

ID AAU78121 standard; protein; 329 AA.

XX AAU78121;

XX 02-JUL-2002 (first entry)

DE Feline CD86 protein.  
 XX  
 XX Cat; vaccine; feline immunodeficiency virus; FIV; immunosuppressant;  
 KW feline infectious peritonitis; CD80 ligand; CD86 ligand; CD28; receptor;  
 KW CTLA-4; vaccine; rabies; autoimmune disease; organ transplant;  
 KW toxoplasmosis gondii; flea; parasite; panleukopenia; feline leukemia;  
 KW FELV; calicivirus; rotavirus; reovirus type 3; coronavirus; herpes;  
 KW borna disease.  
 XX  
 XX Felle sp.  
 OS  
 PN US2002028208-A1.  
 XX  
 XX 07-MAR-2002.  
 PD  
 XX 30-APR-1999; 99US-00303510.  
 PF  
 XX 01-MAY-1998; 98US-0083869P.  
 PR  
 XX (COLL/) COLLISSON E W.  
 PA (HASH/) HASH S M.  
 PA (CHOI/) CHOI I.  
 XX  
 PI Collisson EW, Hash SM, Choi I;  
 DR WPI: 2002-215045/35.  
 DR N-PSDB; AER48230.  
 XX  
 PT Polynucleotide encoding polypeptide of CD80 ligand, CD86 ligand, CD28  
 PT receptor or CTLA-4 receptor as vaccine for inducing immune response in  
 PT feline suffering from autoimmune disease or tissue or organ transplant.  
 PS Disclosure: Fig 3A, 73pp; English.  
 XX  
 XX This invention relates to the DNA and protein sequences encoding a  
 CC soluble CD80 ligand, soluble CD86 ligand, soluble and membrane-bound CD28  
 CC receptor and soluble or membrane bound CTLA-4 receptor. The invention  
 CC also relates to a vaccine comprising an effective amount of these  
 CC receptor proteins. A vaccine is useful for inducing immunity or enhancing  
 CC an immune response in a cat. The protein sequences of the invention are  
 CC useful for suppressing an immune response in a feline suffering from an  
 CC autoimmune disease or the recipient of a tissue or organ transplant. A  
 CC vector containing the DNA sequences of the invention is useful for  
 CC redirecting an immune response in a feline to an immunogen such as rabies  
 CC virus, chlamydia, toxoplasmosis gondii, flea, feline immunodeficiency  
 CC virus, feline leukaemia (FeLV), feline infectious peritonitis virus  
 CC (FIP), panleukopenia virus, calicivirus, reovirus type 3, rotavirus,  
 CC coronavirus, syncytial virus, herpes virus, sarcoma virus, borna disease  
 CC virus or a parasite. The protein sequences may be further utilised to  
 CC promote growth in homologous or heterologous feline species. Enhancement  
 CC of immunity through the interaction of soluble CD80 or soluble CD86 with  
 CC CD28 or CTLA-4 or inhibition of an immune response through the  
 CC interaction of feline CD80 or CD86 with CTLA-4 takes advantage of the  
 CC natural process of regulation rather than adding foreign substances that  
 CC could have multiple, even detrimental effects on overall or long term  
 CC health. The present sequence represents feline CD86 protein of the  
 CC invention  
 XX  
 XX Sequence 329 AA;  
 SQ

Query Match 78.3%; Score 54; DB 5; Length 329;  
 Best Local Similarity 81.8%; Pred. No. 2.6;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 CSSTGYPEPQ 11  
 ||| |||||  
 DB 159 CSSTGYPEPK 169  
 RESULT 11  
 AAY41079  
 ID AAY41079 standard; protein; 332 AA.  
 XX

AC AAY41079;  
 XX  
 DT 20-DEC-1999 (first entry)  
 XX  
 DE Feline B7-2 protein.  
 XX  
 KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;  
 KW allergic reaction; infectious disease; tumor development; feline;  
 KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.  
 XX  
 XX Felis catus.  
 OS  
 PN WO947558-A2.  
 XX  
 XX 23-SEP-1999.  
 PD  
 XX 19-MAR-1999; 99WO-US006187.  
 PF  
 XX 19-MAR-1998; 98US-0078765P.  
 PR 17-APR-1998; 98US-00062597.  
 XX  
 PA (HESK-) HESKA CORP.  
 XX  
 PI Sim G, Yang S, Sellins KS;  
 DR WPI: 1999-571822/48.  
 DR N-PSDB; AA227929, AA227931.  
 XX  
 PT New isolated B7 and CTLA4 nucleic acids, used to develop products for  
 PT treating, e.g. autoimmune and atopic diseases.  
 PS Claim 4; Page 116-119; 148pp; English.  
 XX  
 XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)  
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be  
 CC expressed by standard recombinant methodology. The nucleic acid molecules  
 CC and the encoded proteins can be used for preventing or treating diseases,  
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor  
 CC development, graft rejection, inflammation, arthritis and atopic diseases  
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,  
 CC cats, cattle, sheep or pets. The products can also be used for detection,  
 CC diagnosis and drug screening  
 XX  
 XX Sequence 332 AA;  
 SQ

Query Match 78.3%; Score 54; DB 2; Length 332;  
 Best Local Similarity 81.8%; Pred. No. 2.6;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 CSSTGYPEPQ 11  
 ||| |||||  
 DB 159 CSSTGYPEPK 169  
 RESULT 12  
 ID AAM08473  
 ID AAM08473 standard; protein; 102 AA.  
 XX  
 AC AAM08473;  
 XX  
 DT 08-APR-1997 (first entry)  
 XX  
 DE Human B lymphocyte antigen B7-2 constant region.  
 XX  
 KW CTLA4; CD28; ligand; B7-2; B lymphocyte antigen; B-cell; costimulation;  
 KW immunoglobulin; antibody; autoimmune disease; allergy; tumour; vaccine;  
 KW graft versus host disease; T-cell; T lymphocyte; TH2 response;  
 KW immunosuppressive; immunostimulant; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9640915-A2.  
 XX

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FD 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US000952.
XX
XX 07-JUN-1995; 95US-00479744.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX (REBK ) REPLIGEN CORP.
XX
XX Freeman GJ, Nadler LM, Gray GS;
XX
XX WPI, 1997-077269/07.
XX N-PSDB; AAT49198.
XX
XX DNA encoding a B7-2 fusion protein - used to enhance or down regulate B
XX lymphocyte antigens.
XX
XX Example 7d; Page 124, 171pp; English.
XX
XX A cDNA clone (AAT49198) codes for the constant region-like domain
XX (AA08473) of human B-lymphocyte antigen B7-2 (see also AA08467), a
XX CITA4/CD28 ligand which costimulates T cell activation. It was obt. by
XX PCR amplification (see also AAT49604-05) and cloned into pMRSH/IgG1. B7-
XX 2 constant region-IgG1 constant region fusion protein, B7-2C1g, was
XX expressed in COS and CHO cells. Such fusion proteins can be used to
XX suppress T cell-mediated immune responses
XX
XX Sequence 102 AA;
XX
XX
XX Query Match 73.9%; Score 51; DB 2; Length 102;
XX Best Local Similarity 66.7%; Pred. No. 2.4;
XX Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0
XX
XX 1 CSSTQGYEPKOR 12
XX ||| |||||
XX 24 CSSTHGYPEPKK 35
XX
XX RESULT 13
XX AAB37093
XX ID AAB37093 standard; protein; 102 AA.
XX
XX AAB37093;
XX
XX DT 28-MAR-2001 (first entry)
XX
XX DE Human B7-2 constant domain.
XX
XX
XX Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;
XX antigen; extracellular domain; CITA4; immunoglobulin constant region;
XX immunogenicity; tumor; sarcoma; antigen presenting cell; macrophage;
XX T cell-mediated immune response; transplantation; vaccination;
XX fusion construct.
XX
XX OS Homo sapiens.
XX
XX FN US6130316-A.
XX
XX PD 10-OCT-2000.
XX
XX PE 26-JUL-1994; 94US-00280757.
XX
XX PR 26-JUL-1993; 93US-00101624.
XX PR 19-AUG-1993; 93US-00109393.
XX PR 03-NOV-1993; 93US-00147773.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX (REBK ) REPLIGEN CORP.
XX
XX Freeman GJ, Nadler LM, Gray GS, Greenfield E;
XX
XX WPI, 2000-655681/63.
XX DR N-PSDB; AAC84083.
XX

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|                                                                            |                                                                           |
|----------------------------------------------------------------------------|---------------------------------------------------------------------------|
| XX                                                                         | Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for       |
| PT                                                                         | enhancing or suppressing T cell-mediated immune responses, especially     |
| PT                                                                         | during tissue, skin or organ transplantation, or in graft-versus-host     |
| PT                                                                         | disease.                                                                  |
| PS                                                                         |                                                                           |
| XX                                                                         |                                                                           |
| XX                                                                         | Example 7; Col 105-106; 83pp; English.                                    |
| CC                                                                         | The invention relates to an isolated nucleic acid molecule encoding a     |
| CC                                                                         | fusion protein comprising a first nucleotide sequence encoding a first    |
| CC                                                                         | peptide, and a second nucleotide sequence encoding a second peptide. The  |
| CC                                                                         | first nucleotide sequence hybridizes in 6 X sodium chloride/sodium        |
| CC                                                                         | citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C  |
| CC                                                                         | to a portion of a nucleotide sequence which encodes a human or murine B   |
| CC                                                                         | lymphocyte antigen (B7-2) extracellular domain. The first peptide has the |
| CC                                                                         | ability to bind CD28 or CTLA4. The first peptide has an amino acid        |
| CC                                                                         | sequence that is identical or at least 50% identical with the             |
| CC                                                                         | extracellular domain of a human B7-2 peptide (AA877085). The second       |
| CC                                                                         | peptide is especially an immunoglobulin constant region. This sequence    |
| CC                                                                         | represents the human B7-2 constant domain, used for generating an HB7-    |
| CC                                                                         | 2/19 fusion construct. The nucleic acid molecules are useful in various   |
| CC                                                                         | expression vectors to direct synthesis of the corresponding proteins or   |
| CC                                                                         | peptides in a variety of hosts, particularly eukaryotic cells, e.g.,      |
| CC                                                                         | mammalian or insect cell culture. The nucleic acids are also useful for   |
| CC                                                                         | enhancing the immunogenicity of a mammalian cell, e.g. tumour cell        |
| CC                                                                         | (sarcoma) or an antigen presenting cell (macrophage). The fusion proteins |
| CC                                                                         | or peptides are useful for enhancing or suppressing T cell-mediated       |
| CC                                                                         | immune responses, e.g. in situations of tissue, skin or organ             |
| CC                                                                         | transplantation, or in graft-versus-host disease. The proteins are also   |
| CC                                                                         | useful for enhancing the efficacy of vaccination against a variety of     |
| CC                                                                         | pathogens, and may also be used to upregulate an immune response against  |
| CC                                                                         | a particular pathogen during an infection or against a tumour in a tumour |
| CC                                                                         | -bearing host                                                             |
| SQ                                                                         |                                                                           |
| SQ                                                                         | Sequence 102 AA;                                                          |
| Query Match                                                                | 73.9%; Score 51; DB 3; Length 102;                                        |
| Best Local Similarity                                                      | 66.7%; Pred. No. 2.4;                                                     |
| Matches                                                                    | 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0.                        |
| OY                                                                         | 1 CSSTGQGYEPPOR 12<br>         :<br>Db 24 CSSIHGVPEPKK 35                 |
| RESULT 14                                                                  |                                                                           |
| AAM90209                                                                   |                                                                           |
| ID AAM90209                                                                | standard; protein; 244 AA.                                                |
| AC AAM90209;                                                               |                                                                           |
| XX XX                                                                      |                                                                           |
| DT 10-MAY-1999                                                             | (first entry)                                                             |
| DE hb7.this soluble fusion protein.                                        |                                                                           |
| XX XX                                                                      |                                                                           |
| KM B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;    |                                                                           |
| KM T cell activation; inhibitor; graft versus host disease;                |                                                                           |
| KM transplant rejection; allograft rejection; autoimmune disease; allergy; |                                                                           |
| therapy; human; hb7.this.                                                  |                                                                           |
| XX XX                                                                      |                                                                           |
| OS Homo. sapiens.                                                          |                                                                           |
| OS Synthetic.                                                              |                                                                           |
| OS Chimeric.                                                               |                                                                           |
| FT FT                                                                      | %                                                                         |
| FT Key                                                                     | Location/Qualifiers                                                       |
| FT Peptide                                                                 | 1..23                                                                     |
| FT Domain                                                                  | /note= "potential eukaryotic secretory signal peptide"                    |
| FT                                                                         | 24..238                                                                   |
| FT                                                                         | /note= "human B7.2 (mature protein) extracellular domain"                 |
| FT Peptide                                                                 | 239..244                                                                  |
| FT                                                                         | /note= "histidine detection/purification tag"                             |
| XX XX                                                                      |                                                                           |
| WO9858965-A2.                                                              |                                                                           |

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XX 30-DEC-1998.
PD 22-JUN-1998; 98WO-EP003791.
XX 20-JUN-1997; 97EP-00870092.
XX (INNO-) INNOGENETICS NV.
XX Lorre K, Sablon E, Buyse M, Bosman A;
XX WPI, 1999-105615/09.
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX immune diseases including allograft rejection.
XX Example 3.1.3; Fig 5; 182pp; English.
XX This 28 kDa soluble fusion protein, termed hb7.2his, is composed of human
XX co-stimulatory molecule B7.2 extracellular domain fused C-terminally to a
XX hexahistidine detection/purification tag. It was produced by PCR
XX amplification (see AAX01603-04) of hb7.2 cDNA in pCDNA3.2 (ICG2307),
XX insertion of the PCR fragment into baculovirus transfer vector pAcSG2 and
XX expression in Sf9 Spodoptera frugiperda insect cells. The invention
XX relates to molecules such as diabodies, trivalent and tetravalent
XX antibodies and small antigen binding peptides which can cross-link, or
XX cross-react with, B7.1 and B7.2 expressed on professional antigen
XX presenting cells, leading to the inhibition of antigen-specific T cell
XX activation. Methods to produce such molecules are provided. The molecules
XX are used to treat or prevent diseases of the immune system, in particular
XX graft rejection, graft versus host disease, allergy and autoimmune
XX diseases (claimed)
XX
SQ Sequence 244 AA;
Query Match 73.9%; Score 51; DB 2; Length 244;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CSSTQGYPEPOR 12
Db 151 CSIHGYPEPKK 162
RESULT 15
ID AAW66005 standard; protein; 246 AA.
XX AAW66005;
AC AAW66005;
DT 15-MAR-1999 (first entry)
XX 15-MAR-1999 (first entry)
DE Human B7-2 extracellular domain and linker.
XX Human B7-2 extracellular domain and linker.
KM Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KM monoclonal antibody; single chain antibody; mouse; human; B7-2;
KM co-stimulatory molecule.
XX co-stimulatory molecule.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX Chimeric.
FH Key Location/Qualifiers
FT 1..16
FT /label= Sig_peptide
FT 17..241
FT /label= Mat_protein
FT /note= "B7-2 extracellular domain"
FT 242..246
FT /label= Linker
XX WO9855607-A2.

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PD 10-DEC-1998.
XX 04-JUN-1998; 98WO-GB001627.
XX 04-JUN-1997; 97GB-00011579.
XX 20-JUN-1997; 97GB-00013150.
XX 04-JUL-1997; 97GB-00014230.
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX Kingeman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
XX WPI, 1999-059910/05.
XX N-PSDB; AAW80293.
XX New vector encoding a tumour interacting protein for treating cancer -
XX contains a desired nucleotide sequence and/or protein which recognises
XX tumours, and is used as a gene delivery system to treat cancer.
XX Example 5; Fig 4; 82pp; English.
XX This polypeptide comprises the extracellular domain (amino acids 1-215)
XX of human co-stimulatory molecule B7-2 joined to a C-terminal flexible
XX peptide linker. It is part of B7-2.5T4.1 co-stimulatory domain, a fusion
XX protein comprising the B7-2 extracellular domain joined via the linker to
XX an scFv (see AAW66002) derived from murine 5T4 monoclonal antibody. B7-
XX 2.5T4.1 cDNA (see AAW80293) can be inserted into vector pCI to allow
XX expression of the fusion protein in mammalian cells. The trophoblast cell
XX surface antigen defined by 5T4 is expressed at high levels on the cells
XX of a wide variety of human tumours. The invention relates to a vector
XX comprising a nucleotide sequence coding for a tumour interacting protein
XX (TIP) and optionally a nucleotide sequence of interest (NOI) which
XX encodes a protein of interest (POI), the vector being capable of
XX delivering the NOI and/or POI to the tumour recognised by the TIP.
XX Delivery can be in vivo or ex vivo. The vector is used to treat cancer,
XX and may also be used as a gene delivery system for introducing at least 1
XX CC gene encoding a TIP (preferably a tumour binding protein) into a
XX CC haematopoietic cell lineage. B7-2 is expected to bind specifically to
XX CC CD28 and CTLA-4 present on human T-cells
XX
SQ Sequence 246 AA;
Query Match 73.9%; Score 51; DB 2; Length 246;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CSSTQGYPEPOR 12
Db 151 CSIHGYPEPKK 162

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Search completed: December 15, 2004, 16:37:32  
 Job time : 132.143 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: December 15, 2004, 16:29:06 : Search time 20.5714 seconds  
(without alignments)  
38.685 Million cell updates/sec

Title: US-09-868-605-14\_COPY\_151\_162  
Perfect score: 69  
Sequence: 1 CSSTGYPEPQR 12

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents RA: \*  
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3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
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| 1          | 69    | 100.0       | 325    | 4     | US-09-651-200-20  |
| 2          | 54    | 78.3        | 329    | 4     | US-09-651-200-18  |
| 3          | 54    | 78.3        | 329    | 4     | US-09-651-200-19  |
| 4          | 54    | 78.3        | 329    | 4     | US-09-303-040-6   |
| 5          | 51    | 73.9        | 102    | 3     | US-08-479-744A-47 |
| 6          | 51    | 73.9        | 102    | 3     | US-08-280-757B-47 |
| 7          | 51    | 73.9        | 102    | 3     | US-09-425-762-47  |
| 8          | 51    | 73.9        | 323    | 4     | US-09-651-200-21  |
| 9          | 51    | 73.9        | 323    | 4     | US-09-441-411-22  |
| 10         | 51    | 73.9        | 323    | 5     | PCT-US94-09642-2  |
| 11         | 51    | 73.9        | 324    | 4     | US-09-810-174B-6  |
| 12         | 51    | 73.9        | 324    | 4     | US-09-620-461-6   |
| 13         | 51    | 73.9        | 329    | 2     | US-08-456-104-2   |
| 14         | 51    | 73.9        | 329    | 2     | US-08-101-624-2   |
| 15         | 51    | 73.9        | 329    | 3     | US-08-479-744A-2  |
| 16         | 51    | 73.9        | 329    | 3     | US-08-280-757B-2  |
| 17         | 51    | 73.9        | 329    | 3     | US-08-205-697A-23 |
| 18         | 51    | 73.9        | 329    | 3     | US-08-702-525-23  |
| 19         | 51    | 73.9        | 329    | 3     | US-08-403-253A-4  |
| 20         | 51    | 73.9        | 329    | 4     | US-09-667-135-32  |
| 21         | 51    | 73.9        | 329    | 4     | US-08-435-816A-4  |
| 22         | 51    | 73.9        | 329    | 4     | US-09-425-762-2   |
| 23         | 51    | 73.9        | 329    | 4     | US-09-837-867A-23 |
| 24         | 51    | 73.9        | 329    | 4     | US-09-206-132-2   |
| 25         | 51    | 73.9        | 329    | 4     | US-09-441-411-26  |
| 26         | 51    | 73.9        | 329    | 5     | PCT-US95-02576-23 |
| 27         | 51    | 73.9        | 351    | 4     | US-09-756-983-18  |

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| 28 | 46 | 66.7 | 315 | 4 | US-09-910-174B-28 | Sequence 28, Appl |
| 29 | 46 | 66.7 | 315 | 4 | US-09-620-461-28  | Sequence 28, Appl |
| 30 | 46 | 66.7 | 441 | 4 | US-09-651-200-4   | Sequence 4, Appl  |
| 31 | 46 | 66.7 | 534 | 4 | US-09-651-200-6   | Sequence 6, Appl  |
| 32 | 46 | 66.7 | 534 | 4 | US-09-651-200-24  | Sequence 24, Appl |
| 33 | 44 | 63.8 | 303 | 4 | US-09-651-200-23  | Sequence 15, Appl |
| 34 | 44 | 63.8 | 303 | 4 | US-09-441-411-15  | Sequence 20, Appl |
| 35 | 44 | 63.8 | 303 | 4 | US-09-441-411-20  | Sequence 4, Appl  |
| 36 | 44 | 63.8 | 309 | 2 | US-08-456-104-4   | Sequence 23, Appl |
| 37 | 44 | 63.8 | 309 | 3 | US-08-479-744A-23 | Sequence 23, Appl |
| 38 | 44 | 63.8 | 309 | 3 | US-08-280-757B-23 | Sequence 21, Appl |
| 39 | 44 | 63.8 | 309 | 3 | US-08-205-697A-21 | Sequence 21, Appl |
| 40 | 44 | 63.8 | 309 | 3 | US-08-702-525-21  | Sequence 22, Appl |
| 41 | 44 | 63.8 | 309 | 4 | US-09-651-200-22  | Sequence 23, Appl |
| 42 | 44 | 63.8 | 309 | 4 | US-09-667-135-33  | Sequence 33, Appl |
| 43 | 44 | 63.8 | 309 | 4 | US-09-425-762-23  | Sequence 21, Appl |
| 44 | 44 | 63.8 | 309 | 4 | US-09-837-867A-21 | Sequence 4, Appl  |
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#### ALIGNMENTS

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RESULT 1
US-09-651-200-20
; Sequence 20, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651,200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 325
; TYPE: PRT
; ORGANISM: sus sp.
US-09-651-200-20

Query Match          100.0%; Score 69; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 CSSTGYPEPQR 12
Db      151 CSSTGYPEPQR 162

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US-09-651-200-18
; Sequence 18, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651,200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
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PRIOR FILING DATE: 1999-12-21  
PRIOR APPLICATION NUMBER: 60/183578  
PRIOR FILING DATE: 2000-02-18  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 18  
LENGTH: 329  
TYPE: PRT  
ORGANISM: Felis catus  
US-09-651-200-18

Query Match 78.3%; Score 54; DB 4; Length 329;  
Best Local Similarity 81.8%; Pred. No. 0.36;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11  
DB 159 CSSTQGYPEPK 169

RESULT 3  
US-09-651-200-19  
Sequence 19, Application US/09651200  
Patent No. 6429303  
GENERAL INFORMATION:  
APPLICANT: Green et al  
TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
TITLE OF INVENTION: Polypeptides Encoded Thereby  
FILE REFERENCE: 15966-562 (CURA-62)  
CURRENT APPLICATION NUMBER: US/09/651,200  
PRIOR FILING DATE: 2000-08-30  
PRIOR APPLICATION NUMBER: 60/152383  
PRIOR FILING DATE: 1999-09-03  
PRIOR APPLICATION NUMBER: 60/172909  
PRIOR FILING DATE: 1999-12-21  
PRIOR APPLICATION NUMBER: 60/183578  
PRIOR FILING DATE: 2000-02-18  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 19  
LENGTH: 329  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-09-651-200-19

Query Match 78.3%; Score 54; DB 4; Length 329;  
Best Local Similarity 81.8%; Pred. No. 0.36;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11  
DB 158 CSSTQGYPEPK 168

RESULT 4  
US-09-303-040-6  
Sequence 6, Application US/09303040  
Patent No. 6555671  
GENERAL INFORMATION:  
APPLICANT: Winslow, Barbara J.  
TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding  
TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CTLA-4 or  
TITLE OF INVENTION: Feline Interferon-gamma And Uses Thereof  
FILE REFERENCE: 54957-B  
CURRENT APPLICATION NUMBER: US/09/303,040  
PRIOR FILING DATE: 1999-04-30  
EARLIER APPLICATION NUMBER: 60/083,870  
PRIOR FILING DATE: 1998-05-01  
NUMBER OF SEQ ID NOS: 82  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6

LENGTH: 329  
TYPE: PRT  
ORGANISM: feline CD86  
US-09-303-040-6

Query Match 78.3%; Score 54; DB 4; Length 329;  
Best Local Similarity 81.8%; Pred. No. 0.36;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11  
DB 159 CSSTQGYPEPK 169

RESULT 5  
US-08-479-744A-47  
Sequence 47, Application US/08479744A  
Patent No. 6084067  
GENERAL INFORMATION:  
APPLICANT: Freeman, Gordon J.  
APPLICANT: Nadler, Lee M.  
APPLICANT: Gray, Gary S.  
TITLE OF INVENTION: No. 6084067e1 CTLA4/CD28 Ligands and  
TITLE OF INVENTION: Uses Therefor  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,744A  
FILING DATE: June 7, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/280,757  
FILING DATE: 26-JUL-1994  
APPLICATION NUMBER: 08/109,393  
FILING DATE: 28-AUG-1993  
APPLICATION NUMBER: 08/101,624  
FILING DATE: 26-JULY-1993  
APPLICATION NUMBER: 08/147,773  
FILING DATE: 3-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragoras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-004CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 102 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-479-744A-47

Query Match 73.9%; Score 51; DB 3; Length 102;  
Best Local Similarity 66.7%; Pred. No. 0.34;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 12  
DB 24 CSSTQGYPEPK 35

Page 3

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1 STREET: 60 State Street
2 CITY: Boston
3 STATE: Massachusetts
4 COUNTRY: USA
5 ZIP: 02109
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 OPERATING SYSTEM: IBM PC compatible
10 SOFTWARE: PatentIn Release #1.0, Version #1.25
11
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/09/425,762
14 FILING DATE:
15 CLASSIFICATION:
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 08/479,744
18 FILING DATE:
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Mardigouras, Amy E.
21 REGISTRATION NUMBER: 36,207
22 REFERENCE/DOCKET NUMBER: RPI-004CP3
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (617) 227-7400
25 TELEFAX: (617) 227-5941
26 INFORMATION FOR SEQ. ID NO.: 47:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 102 amino acids
29 TYPE: amino acid
30 TOPOLOGY: linear
31 MOLECULE TYPE: protein
32
33 US-09-425-762-47
34
35 Query Match 73.9%; Score 51; DB 4; Length 102;
36 Best Local Similarity 66.7%; Pred. NO. 0.34;
37 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
38
39 QY 1 CSSTOGEPEPOR 12
40 ||| |||||:
41
42 Db 24 CSSTHGPPEPK 35
43
44 RESULT 8
45 US-09-651-200-21
46 Sequence 21, Application US/09651200
47 Patent No. 6429303
48 GENERAL INFORMATION:
49 APPLICANT: Green et al
50 TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
51 TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
52 FILE REFERENCE: 15966-562 (CURA-62)
53 CURRENT APPLICATION NUMBER: US/09/651,200
54 CURRENT FILING DATE: 2000-08-30
55 PRIOR APPLICATION NUMBER: 60/152383
56 PRIOR FILING DATE: 1999-09-03
57 PRIOR APPLICATION NUMBER: 60/172909
58 PRIOR FILING DATE: 1999-12-21
59 PRIOR APPLICATION NUMBER: 60/183578
60 PRIOR FILING DATE: 2000-02-18
61 NUMBER OF SEQ. ID NOS: 25
62 SOFTWARE: PatentIn Ver. 2.0
63 SEQ ID NO 21
64 LENGTH: 323
65 TYPE: PRT
66 ORGANISM: Homo sapiens
67
68 US-09-651-200-21
69
70 Query Match 73.9%; Score 51; DB 4; Length 323;
71 Best Local Similarity 66.7%; Pred. NO. 1.1;
72 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
73
74 QY 1 CSSTOGEPEPOR 12
75 ||| |||||:
76
77 Db 1 CSSTHGPPEPK 35

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Db 151 CSISNGYPEPKK 162

## RESULT 9

US-09-441-411-22  
Sequence 22, Application US/0944111  
Patent No. 6734172  
GENERAL INFORMATION:  
APPLICANT: Scholler, Nathalie B.  
APPLICANT: Disis, Mary L.  
APPLICANT: Helstrom, Ingegerd  
APPLICANT: Helstrom, Karl Erik  
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES  
FILE REFERENCE: 730033.409  
CURRENT APPLICATION NUMBER: US/09/441.411  
CURRENT FILING DATE: 1999-11-16  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 22  
LENGTH: 323  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-441-411-22

## Query Match

Best Local Similarity 73.9%; Score 51; DB 4; Length 323;  
Best Local Similarity 66.7%; Pred. No. 1.1;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSSTQGYPEPKR 12

Db 151 CSISNGYPEPKK 162

## RESULT 10

PCT-US94-09642-2  
Sequence 2, Application PC/TUS9409642  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Purified Mammalian CTLA-4 Binding  
TITLE OF INVENTION: Protein and Related Reagents  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: Schering-Plough Corporation, M-3-W  
STREET: One Giralda Farms  
CITY: Madison  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07940-1000  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh IICx  
OPERATING SYSTEM: System Software 7.1  
SOFTWARE: Microsoft Word 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09642  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/120,606  
FILING DATE: 13-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/116,882  
FILING DATE: 03-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Blaisdale, John H. C.  
REGISTRATION NUMBER: 31,895  
REFERENCE/DOCKET NUMBER: EX0390X1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-822-7398  
TELEFAX: 201-822-7039  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 323 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-09642-2

## Query Match

Best Local Similarity 73.9%; Score 51; DB 5; Length 323;  
Best Local Similarity 66.7%; Pred. No. 1.1;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSSTQGYPEPKR 12

Db 151 CSISNGYPEPKK 162

## RESULT 11

US-09-910-174B-6  
Sequence 6, Application US/09910174B  
Patent No. 6630575  
GENERAL INFORMATION:  
APPLICANT: Coyle, Anthony J.  
APPLICANT: Frazer, Christopher C.  
APPLICANT: Manning, Stephen  
TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7  
TITLE OF INVENTION: Family and Uses Thereof  
FILE REFERENCE: 35800/236924  
CURRENT APPLICATION NUMBER: US/09/910,174B  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 09/620,461  
PRIOR FILING DATE: 2000-07-20  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 324  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-910-174B-6

## Query Match

Best Local Similarity 73.9%; Score 51; DB 4; Length 324;  
Best Local Similarity 66.7%; Pred. No. 1.1;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSSTQGYPEPKR 12

Db 151 CSISNGYPEPKK 162

## RESULT 12

US-09-620-461-6  
Sequence 6, Application US/09620461  
Patent No. 6635750  
GENERAL INFORMATION:  
APPLICANT: Coyle, Anthony J.  
APPLICANT: Frazer, Christopher C.  
APPLICANT: Manning, Stephen  
TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7  
TITLE OF INVENTION: Family and Uses Thereof  
FILE REFERENCE: 5800-149  
CURRENT APPLICATION NUMBER: US/09/620,461  
CURRENT FILING DATE: 2000-07-20  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 324  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-620-461-6

## Query Match

Best Local Similarity 73.9%; Score 51; DB 4; Length 324;  
Best Local Similarity 66.7%; Pred. No. 1.1;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSSTQGYPEPKR 12

Db 151 CSISNGYPEPKK 162



Db 151 CSSTGYPEPK 162

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RESULT 13
US-08-456-104-2
; Sequence 2, Application US/08456104
; Patent No. 5861310
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,104
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624;
; FILING DATE: 26-JUL-1993;
; APPLICATION NUMBER: 08/109,393;
; APPLICATION NUMBER: 19-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-456-104-2

Query Match 73.9%; Score 51; DB 2; Length 329;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPK 12
Db 157 CSSTGYPEPK 168

RESULT 14
US-08-101-624-2
; Sequence 2, Application US/08101624
; Patent No. 5942607
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 5942607el CTLA4/CD28 ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
```

```
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/101,624
; FILING DATE: 26-JUL-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-101-624-2
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Query Match 73.9%; Score 51; DB 2; Length 329;  
Best Local Similarity 66.7%; Pred. No. 1.1;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPK 12  
Db 157 CSSTGYPEPK 168

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RESULT 15
US-08-479-744A-2
; Sequence 2, Application US/08479744A
; Patent No. 6084067
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 6084067el CTLA4/CD28 ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,744A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/280,757
; FILING DATE: 26-JUL-1994
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 28-AUG-1993
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
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APPLICATION NUMBER: 08/147,773  
FILING DATE: 3-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Maniagouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-004CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 329 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-479-744A-2

Query Match 73.9%, Score 51, DB 3, Length 329,  
Best Local Similarity 66.7%, Pred. No. 1.1,  
Matches 8, Conservative 2, Mismatches 2, Indels 0, Gaps 0;

CY 1 CSSTQGYPEPOR 12  
||| |||||:  
Db 157 CSSTHGYPEPKK 168

Search completed: December 15, 2004, 16:38:41  
Job time : 20.5714 secs



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RESULT 2
US-09-303-510-6
; Sequence 6, Application US/09303510A
; Patent No. US20020028208A1
; GENERAL INFORMATION:
; APPLICANT: Collisson, Ellen W.
; APPLICANT: Hash, Stephen M.
; APPLICANT: Choi, Insoo
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline
; FILE REFERENCE: 54354
; CURRENT APPLICATION NUMBER: US/09/303,510A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,869
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Feline
US-09-303-510-6

Query Match
Best Local Similarity 78.3%; Score 54; DB 9; Length 329;
Best Local Similarity 81.8%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTOQYPEPQ 11
DB 159 CSSTOQYPEPK 169

RESULT 3
US-09-303-040-6
; Sequence 6, Application US/09303040
; Patent No. US20020051792A1
; GENERAL INFORMATION:
; APPLICANT: Winslow, Barbara J.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or
; FILE REFERENCE: 54957-B
; CURRENT APPLICATION NUMBER: US/09/303,040
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,870
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Feline CD86
US-09-303-040-6

Query Match
Best Local Similarity 78.3%; Score 54; DB 9; Length 329;
Best Local Similarity 81.8%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTOQYPEPQ 11
DB 159 CSSTOQYPEPK 169

RESULT 4
US-10-790-396-7
; Sequence 7, Application US/10790396
; Publication No. US20040157296A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Sellins, Karen S.
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
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; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-1-C1-PCT
; CURRENT APPLICATION NUMBER: US/10/790,396
; CURRENT FILING DATE: 2004-03-01
; PRIOR APPLICATION NUMBER: 60/078,765
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/078,765
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 09/062,597
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-790-396-7

Query Match
Best Local Similarity 78.3%; Score 54; DB 16; Length 329;
Best Local Similarity 81.8%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTOQYPEPQ 11
DB 158 CSSTOQYPEPK 168

RESULT 5
US-10-790-396-26
; Sequence 26, Application US/10790396
; Publication No. US20040157296A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Sellins, Karen S.
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-1-C1-PCT
; CURRENT APPLICATION NUMBER: US/10/790,396
; CURRENT FILING DATE: 2004-03-01
; PRIOR APPLICATION NUMBER: US/09/646,561
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/078,765
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 09/062,597
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Felis catus
US-10-790-396-26

Query Match
Best Local Similarity 78.3%; Score 54; DB 16; Length 332;
Best Local Similarity 81.8%; Pred. No. 1.4;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTOQYPEPQ 11
DB 159 CSSTOQYPEPK 169

RESULT 6
US-09-425-762-47
; Sequence 47, Application US/09425762
; Publication No. US20020086414A1
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 6605279e1 CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
```

NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/425,762  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,744  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragoras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-004CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 102 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-425-762-47

Query Match 73.9%; Score 51; DB 9; Length 102;  
Best Local Similarity 66.7%; Pred. No. 1.3;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPOR 12  
DB 24 CSIHGYPEPKX 35

RESULT 7  
US-09-915-789A-22  
Sequence 22, Application US/09915789A  
Patent No. US20020168762A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Lieping  
TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY  
FILE OF INVENTION: MOLECULES  
FILE REFERENCE: 07035-219001  
CURRENT APPLICATION NUMBER: US/09/915,789A  
CURRENT FILING DATE: 2002-06-04  
PRIOR APPLICATION NUMBER: US 60/220,991  
PRIOR FILING DATE: 2000-07-27  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 22  
LENGTH: 219  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-915-789A-22

Query Match 73.9%; Score 51; DB 9; Length 219;  
Best Local Similarity 66.7%; Pred. No. 2.8;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPOR 12  
DB 129 CSIHGYPEPKX 140

RESULT 8  
US-10-334-235-40  
Sequence 40, Application US/10334235  
Publication No. US20040131591A1  
GENERAL INFORMATION:  
APPLICANT: Oxford Biomedica (UK) Ltd.  
APPLICANT: Kingsman, Alan  
APPLICANT: Bebbington, Christopher  
APPLICANT: Carroll, Miles  
APPLICANT: Ellard, Fiona  
APPLICANT: Kingsman, Susan  
APPLICANT: Myers, Kevin  
APPLICANT: Lamikandra, Abigail  
TITLE OF INVENTION: VECTOR SYSTEM  
FILE REFERENCE: 532682000920  
CURRENT APPLICATION NUMBER: US/10/334,235  
CURRENT FILING DATE: 2002-12-30  
PRIOR APPLICATION NUMBER: US 10/060,585  
PRIOR FILING DATE: 2002-01-29  
PRIOR APPLICATION NUMBER: PCT/GB00/04317  
PRIOR FILING DATE: 2000-11-13  
PRIOR APPLICATION NUMBER: US 09/445,375  
PRIOR FILING DATE: 1998-06-04  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 40  
LENGTH: 246  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-334-235-40

Query Match 73.9%; Score 51; DB 16; Length 246;  
Best Local Similarity 66.7%; Pred. No. 3.1;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPOR 12  
DB 151 CSIHGYPEPKX 162

RESULT 9  
US-09-845-899A-5  
Sequence 5, Application US/09845899A  
Patent No. US20020147326A1  
GENERAL INFORMATION:  
APPLICANT: CHAIKIN, MARGERY ANN  
APPLICANT: LYNN, SALLY DOREEN PATRICIA  
APPLICANT: SWEET, RAYMOND W.  
APPLICANT: TRUENH, ALEMESEGED  
TITLE OF INVENTION: HEXAMERIC FUSION PROTEINS AND USES  
FILE OF INVENTION: THEREFOR  
FILE REFERENCE: P50496  
CURRENT APPLICATION NUMBER: US/09/845,899A  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: 09/202,346  
PRIOR FILING DATE: 1999-01-13  
PRIOR APPLICATION NUMBER: US 60/043,948  
PRIOR FILING DATE: 1997-02-19  
PRIOR APPLICATION NUMBER: US 60/038,915  
PRIOR FILING DATE: 1997-02-21  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 260  
TYPE: PRT  
ORGANISM: HOMO SAPIENS  
US-09-845-899A-5

Query Match 73.9%; Score 51; DB 9; Length 260;  
Best Local Similarity 66.7%; Pred. No. 3.3;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTOGEPEPQR 12  
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Db 157 CSIHGYPEPKK 168

RESULT 10  
US-09-955-866-5  
; Sequence 5, Application US/09955866  
; Patent No. US20020107363A1  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Michael  
; APPLICANT: Sullivan, John K.  
; APPLICANT: Holst, Paige  
; APPLICANT: Yoshinaga, Steven Kiyoshi  
; TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof  
; FILE REFERENCE: 00,759-A  
; CURRENT APPLICATION NUMBER: US/09/955,866  
; CURRENT FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: 60/233,867  
; PRIOR FILING DATE: 2000-09-20  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 323  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-955-866-5

Query Match 73.9%; Score 51; DB 9; Length 323;  
Best Local Similarity 66.7%; Pred. No. 4.1;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTOGEPEPQR 12  
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Db 151 CSIHGYPEPKK 162

RESULT 11  
US-09-896-738-11  
; Sequence 11, Application US/09896738  
; Patent No. US20020165347A1  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Michael  
; APPLICANT: Sullivan, John K.  
; APPLICANT: Fang, Mel  
; TITLE OF INVENTION: B7-Like Molecules and Uses Thereof  
; FILE REFERENCE: 00-513-A  
; CURRENT APPLICATION NUMBER: US/09/896,738  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 60/215,645  
; PRIOR FILING DATE: 2000-06-30  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 323  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-896-738-11

Query Match 73.9%; Score 51; DB 9; Length 323;  
Best Local Similarity 66.7%; Pred. No. 4.1;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTOGEPEPQR 12  
||| |||  
Db 151 CSIHGYPEPKK 162

RESULT 12  
US-09-915-789A-16  
; Sequence 16, Application US/09915789A  
; Patent No. US20020168762A1  
; GENERAL INFORMATION:

APPLICANT: Chen, Lieping  
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY  
; FILE REFERENCE: 07039-219001  
; CURRENT APPLICATION NUMBER: US/09/915,789A  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US 60/220,991  
; PRIOR FILING DATE: 2000-07-27  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 323  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-915-789A-16

Query Match 73.9%; Score 51; DB 9; Length 323;  
Best Local Similarity 66.7%; Pred. No. 4.1;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTOGEPEPQR 12  
||| |||  
Db 151 CSIHGYPEPKK 162

RESULT 13  
US-09-441-411-22  
; Sequence 22, Application US/09441411  
; Publication No. US20030008342A1  
; GENERAL INFORMATION:  
; APPLICANT: Scholler, Nathalie B.  
; APPLICANT: Disis, Mary L.  
; APPLICANT: Hellstrom, Ingegerd  
; APPLICANT: Hellstrom, Karl Erik  
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES  
; FILE REFERENCE: 730033,409  
; CURRENT APPLICATION NUMBER: US/09/441,411  
; CURRENT FILING DATE: 1999-11-16  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 323  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-441-411-22

Query Match 73.9%; Score 51; DB 10; Length 323;  
Best Local Similarity 66.7%; Pred. No. 4.1;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTOGEPEPQR 12  
||| |||  
Db 151 CSIHGYPEPKK 162

RESULT 14  
US-10-087-192-1080  
; Sequence 1080, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 2059  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1080  
; LENGTH: 323  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-087-192-1080

Query Match 73.9%; Score 51; DB 13; Length 323;  
Best Local Similarity 66.7%; Pred. No. 4.1;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPQR 12  
||| |||||:  
Db 151 CSIHGYPEPKK 162

RESULT 15  
US-10-207-655-121  
; Sequence 121, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 121  
; LENGTH: 323  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-207-655-121

Query Match 73.9%; Score 51; DB 14; Length 323;  
Best Local Similarity 66.7%; Pred. No. 4.1;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPQR 12  
||| |||||:  
Db 151 CSIHGYPEPKK 162

Search completed: December 15, 2004, 16:54:14  
Job time: 117.571 secs

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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:28:26 / Search time 14.2857 Seconds  
(without alignments)  
80.822 Million cell updates/sec

Title: US-09-868-605-14\_COPY\_151\_162  
Perfect score: 69  
Sequence: 1 CSSTGQYEPFQR 12

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: PIR 79: \*  
1: PIR: \*  
2: PIR: \*  
3: PIR: \*  
4: PIR: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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|------------|-------|-------------|--------|----|--------|--------------------|
| 1          | 57    | 82.6        | 330    | 2  | I46691 | CD86 precursor - r |
| 2          | 51    | 73.9        | 275    | 2  | JC7604 | CD86 spliced varia |
| 3          | 51    | 73.9        | 328    | 1  | A48754 | B7-2 antigen - hum |
| 4          | 44    | 63.8        | 309    | 2  | I49522 | gene B7-2 protein  |
| 5          | 44    | 63.8        | 579    | 2  | T30635 | hypothetical prote |
| 6          | 42    | 60.9        | 92     | 2  | T18731 | hypothetical prote |
| 7          | 42    | 60.9        | 239    | 2  | I46690 | CD80 precursor - r |
| 8          | 42    | 60.9        | 487    | 2  | S65133 | butyrophilin - mou |
| 9          | 41    | 59.4        | 288    | 2  | A4803  | B-cell-restricted  |
| 10         | 41    | 59.4        | 288    | 2  | G00031 | B7 protein - red-c |
| 11         | 41    | 59.4        | 526    | 2  | S70587 | butyrophilin precu |
| 12         | 41    | 59.4        | 526    | 2  | A37821 | butyrophilin - bov |
| 13         | 40    | 58.0        | 423    | 2  | T29549 | hypothetical prote |
| 14         | 40    | 58.0        | 1273   | 2  | T42405 | sax-3 protein - Ca |
| 15         | 39    | 56.5        | 215    | 2  | C48150 | hibernation-relate |
| 16         | 39    | 56.5        | 323    | 2  | AF0744 | conserved hypotet  |
| 17         | 39    | 56.5        | 470    | 2  | T15196 | hypothetical prote |
| 18         | 39    | 56.5        | 827    | 2  | S59121 | SOX6 protein - mou |
| 19         | 38    | 55.1        | 100    | 2  | F95897 | hypothetical prote |
| 20         | 38    | 55.1        | 142    | 2  | S56414 | hypothetical 16k p |
| 21         | 38    | 55.1        | 142    | 2  | S91274 | hypothetical prote |
| 22         | 38    | 55.1        | 142    | 2  | E86115 | hypothetical prote |
| 23         | 38    | 55.1        | 164    | 2  | T15525 | hypothetical prote |
| 24         | 38    | 55.1        | 307    | 2  | S04923 | homeotic protein H |
| 25         | 38    | 55.1        | 374    | 2  | T51863 | probable RNA bindi |
| 26         | 38    | 55.1        | 378    | 2  | E86226 | hypothetical prote |
| 27         | 38    | 55.1        | 378    | 2  | T52072 | hypothetical prote |
| 28         | 38    | 55.1        | 841    | 2  | T01046 | hypothetical prote |
| 29         | 38    | 55.1        | 1040   | 2  | A57638 | receptor tyrosine  |

|    |    |      |      |   |        |                    |
|----|----|------|------|---|--------|--------------------|
| 30 | 38 | 55.1 | 1103 | 2 | T22899 | hypothetical prote |
| 31 | 38 | 55.1 | 1747 | 2 | A54121 | collagen alpha-4 c |
| 32 | 38 | 55.1 | 1906 | 1 | S68235 | myosin-light-chain |
| 33 | 38 | 55.1 | 2715 | 2 | T13049 | eyelid - fruit fly |
| 34 | 37 | 53.6 | 92   | 2 | T15501 | hypothetical prote |
| 35 | 37 | 53.6 | 207  | 1 | PUPG   | neuroendocrine pro |
| 36 | 37 | 53.6 | 210  | 2 | A49745 | neuroendocrine pro |
| 37 | 37 | 53.6 | 212  | 1 | FUHU   | neuroendocrine pro |
| 38 | 37 | 53.6 | 212  | 2 | S12477 | neuroendocrine pro |
| 39 | 37 | 53.6 | 219  | 2 | A82498 | CdbY family protei |
| 40 | 37 | 53.6 | 237  | 2 | T36722 | probable membrane  |
| 41 | 37 | 53.6 | 259  | 2 | AE3411 | hypothetical prote |
| 42 | 37 | 53.6 | 301  | 2 | G83182 | hypothetical prote |
| 43 | 37 | 53.6 | 379  | 2 | A35669 | Gene CYR61 protein |
| 44 | 37 | 53.6 | 391  | 2 | T09058 | butyrophilin homol |
| 45 | 37 | 53.6 | 431  | 2 | T38471 | probable chromatin |

## ALIGNMENTS

RESULT 1  
146691  
CD86 precursor - rabbit  
C.Species: Oryctolagus cuniculus (domestic rabbit)  
C.Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 09-Jul-2004  
C.Accession: I46691  
R.Isono, T.; Seto, A.  
Immunogenetics 42, 217-220, 1995  
A.Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecu  
A.Reference number: I46689; MUID:95369849; PMID:7642234  
A.Accession: I46691  
A.Status: preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: mRNA  
A.Residues: 1-330 <ISO>  
A.Reference: UNIPROT:P42071; GB:D49842; NID:9755098; PIDN:BA00642.1; PID:975509  
C.Superfamily: B7-2 antigen

Query Match 82.6%; Score 57; DB 2; Length 330;  
Best Local Similarity 75.0%; Pred. No. 0.036;  
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTGQYEPFQR 12  
DB 157 CSSTGQYEPFQR 168

## RESULT 2

UC7604  
CD86 spliced variant CD86 deltaTM isoform - human  
C.Species: Homo sapiens (man)  
C.Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 18-Nov-2002  
C.Accession: UC7604

R.Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeanmin, P.; Bonnefoy, J.Y.; Delneste, Y.  
Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001  
A.Title: Identification of an alternatively spliced variant of human CD86 mRNA.  
A.Reference number: UC7604; MUID:21092744; PMID:11162656  
A.Accession: UC7604

A.Molecule type: mRNA  
A.Residues: 1-275 <MA>  
A.Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory  
C.Genetics:  
A.Gene: cd86deltaTM  
A.Superfamily: B-Lymphocyte restricted antigen B7  
C.Keywords: immune response

Query Match 73.9%; Score 51; DB 2; Length 275;  
Best Local Similarity 66.7%; Pred. No. 0.32;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGQYEPFQR 12  
DB 151 CSSTGQYEPFQR 162

## RESULT 3

A48754  
B7-2 antigen - human  
N/Alternate names: B70 glycoprotein, CD86 antigen, CTLA-4 counter-receptor  
C/Species: Homo sapiens (man)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: A48754; S39055  
R/Freeform: G.J.; Gribben, J.G.; Boussiotis, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombard, Science 262, 909-911, 1993  
A/Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell proliferation  
A/Reference number: A48754; MUID:94053735; PMID:7694363  
A/Accession: A48754  
A/Molecule type: mRNA  
A/Status: preliminary  
A/Residues: 1-329 <FR>  
A/Cross-references: UNIPROT:P42081; GB:L25259; NID:G416368; PIDN:AAA58389.1; PID:G416368  
A/Note: It is uncertain whether Met-1 or Met-7 is the initiator  
R/Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza, C. Nature 366, 76-79, 1993  
A/Title: B70 antigen is a second ligand for CTLA-4 and CD28.  
A/Reference number: S39055; MUID:94050123; PMID:7694153  
A/Accession: S39055  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 7-329 <AZ>  
A/Cross-references: GB:U04343; NID:G439838; PIDN:AAH0314.1; PID:G439839  
C/Genetics:  
A/Gene: GDB:CD86; CD28LG2  
A/Cross-references: GDB:433597; OMIM:601020  
A/Map position: 3q13.3-q21  
C/Superfamily: B7-2 antigen  
C/Keywords: glycoprotein

## Query Match

Best Local Similarity 73.9%; Score 51; DB 1; Length 329;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEP 12

DB 157 CSSTGYPEP 168

## RESULT 4

149522  
gene B7-2 protein - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: 149522  
R/Freeform: G.J.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim, J. Exp. Med. 178, 2185-2192, 1993  
A/Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell proliferation  
A/Reference number: 149522; MUID:9405585; PMID:7504055  
A/Accession: 149522  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-309 <RE>  
A/Cross-references: UNIPROT:P42082; GB:L25506; NID:G432478; PIDN:AAA79770.1; PID:G432478  
C/Genetics:  
A/Gene: B7-2  
C/Superfamily: B7-2 antigen

## Query Match

Best Local Similarity 63.8%; Score 44; DB 2; Length 309;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTGYPEP 12

DB 157 CSSTGYPEP 168

## RESULT 5

T30635  
hypothetical protein 33L - Molluscum contagiosum virus 1

N/Alternate names: MC033L  
C/Species: Molluscum contagiosum virus 1  
C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
C/Accession: T30635  
R/Sankovich, T.G.; Bugert, J.J.; Steller, J.R.; Koonin, E.V.; Darai, G.; Moss, B. Science 273, 813-816, 1996  
A/Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host restriction enzymes  
A/Reference number: Z28076; MUID:96325459; PMID:8670425  
A/Accession: T30635  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-579 <SE>  
A/Cross-references: UNIPROT:Q98201; EMBL:U60315; NID:G1491943; PIDN:AAC55161.1; PID:G1491943  
C/Genetics:  
A/Note: MC033L  
C/Superfamily: Molluscum contagiosum virus 1 hypothetical protein 33L

## Query Match

Best Local Similarity 63.8%; Score 44; DB 2; Length 579;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEP 10

DB 116 CSSTGYPEP 125

## RESULT 6

T18731  
hypothetical protein B0391.10 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T18731  
R/Gardner, A. submitted to the EMBL Data Library, November 1996  
A/Reference number: Z19012  
A/Accession: T18731  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-92 <ML>  
A/Cross-references: UNIPROT:Q62015; EMBL:Z81454; PIDN:CAB03802.1; GSPDB:GN00023; CESP:B0391  
A/Experimental source: clone B0391  
C/Genetics:  
A/Gene: CESP:B0391.10  
A/Map position: 5  
A/Introns: 18/1

## Query Match

Best Local Similarity 60.9%; Score 42; DB 2; Length 92;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEP 10

DB 35 CSSTGYPEP 44

## RESULT 7

146690  
CD80 precursor - rabbit  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 09-Jul-2004  
C/Accession: 146690  
R/Isono, T.; Seto, A. Immunogenetics 42, 217-220, 1995  
A/Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule CD80  
A/Reference number: 146689; MUID:95369849; PMID:7642234  
A/Accession: 146690  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-299 <ISO>  
A/Cross-references: UNIPROT:P42070; GB:D49843; NID:G755096; PIDN:BAA08643.1; PID:G755096  
C/Superfamily: B-lymphocyte restricted antigen B7

Query Match 60.9%; Score 42; DB 2; Length 299;  
 Best Local Similarity 54.5%; Pred. No. 12;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTGYPEPQ 11  
 ||:|||||  
 DB 161 CSASGCFPEPR 171

## RESULT 8

butyrophilin - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 15-Mar-2004  
 C/Accession: S65133  
 R/Smith, T.; Aoki, N.; Noda, A.; Adachi, T.; Nakamura, R.; Matsuda, T.  
 Biochim. Biophys. Acta 1245, 285-292, 1995  
 A/Title: Carboxy-terminal cytoplasmic domain of mouse butyrophilin specifically associat  
 A/Reference number: S65133; MUID:96125722; PMID:8541302  
 A/Accession: S65133  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-487 <ISH>  
 A/Cross-references: GB:S80642; NID:G1246078; PIDN:AA835893.1; PID:G1246079  
 C/Superfamily: rfp transforming protein

Query Match 60.9%; Score 42; DB 2; Length 487;  
 Best Local Similarity 63.6%; Pred. No. 20;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPQ 11  
 ||:|||||  
 DB 128 CTSAGWPEPQ 138

## RESULT 9

A45803  
 B-cell-restricted antigen B7 precursor - human  
 N/Alternate names: B-lymphocyte activation antigen B7  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
 C/Accession: I54495; A45803  
 R/Selvakumar, A.; Mohanraj, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.  
 Immunogenetics 36, 175-181, 1992  
 A/Title: Genomic organization and chromosomal location of the human gene encoding the B-  
 A/Reference number: I54495; MUID:92307753; PMID:1177173  
 A/Accession: I54495  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-288 <RES>  
 R/Freeeman, G.J.; Freedman, A.S.; Segli, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.  
 J. Immunol. 143, 2714-2722, 1989  
 A/Title: B7, a new member of the Ig superfamily with unique expression on activated and  
 A/Reference number: A45803; MUID:90010147; PMID:2794510  
 A/Accession: A45803  
 A/Molecule type: mRNA  
 A/Residues: 1-288 <PRE>  
 A/Cross-references: GB:M27533; NID:G184680; PIDN:AAA36045.1; PID:G306916  
 C/Genetics:  
 A/Gene: GDB:CD80, CD28LG1, CD28  
 A/Cross-references: GDB:251792; OMIM:112203  
 A/Map position: 3q13.3-3q21  
 A/Introns: 34/1; 140/1; 234/1; 266/1  
 C/Superfamily: B-lymphocyte restricted antigen B7  
 C/Keywords: transmembrane protein  
 F:1-26/Domain: signal sequence #status predicted <SIG>  
 F:246-264/Domain: transmembrane #status predicted <TM>

Query Match 59.4%; Score 41; DB 2; Length 288;  
 Best Local Similarity 60.0%; Pred. No. 17;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTGYPEP 10  
 ||:|||||  
 DB 162 CTSAGCFPEPR 171

## RESULT 10

G00031  
 B7 protein - red-crowned mangabey (fragment)  
 C/Species: Cercopithecus torquatus (red-crowned mangabey, white-collared mangabey)  
 C/Date: 11-Apr-1997 #sequence\_revision 11-Apr-1997 #text\_change 09-Jul-2004  
 C/Accession: G00031  
 R/Villinger, F.J.  
 submitted to the EMBL Data Library, January 1995  
 A/Reference number: G00217  
 A/Accession: G00031  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-289 <VIL>  
 A/Cross-references: UNIPROT:Q28347; EMBL:U19833; NID:G644783; PIDN:AAA6700.1; PID:G644  
 C/Genetics:  
 A/Gene: B7  
 C/Superfamily: B-lymphocyte restricted antigen B7

Query Match 59.4%; Score 41; DB 2; Length 289;  
 Best Local Similarity 60.0%; Pred. No. 17;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTGYPEP 10  
 ||:|||||  
 DB 162 CTSAGCFPEPR 171

## RESULT 11

S70587  
 butyrophilin precursor - human  
 C/Species: Homo sapiens (man)  
 C/Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S70587  
 R/Taylor, M.R.; Peterson, J.A.; Ceriani, R.L.; Couto, J.R.  
 Biochim. Biophys. Acta 1306, 1-4, 1995  
 A/Title: Cloning and sequence analysis of human butyrophilin reveals a potential recept  
 A/Reference number: S70587; MUID:96201696; PMID:8611614  
 A/Accession: S70587  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-526 <TAY>  
 A/Cross-references: UNIPROT:Q13410; EMBL:U39576; NID:G1326082; PIDN:AA650489.1; PID:G13  
 C/Superfamily: rfp transforming protein

Query Match 59.4%; Score 41; DB 2; Length 526;  
 Best Local Similarity 63.6%; Pred. No. 32;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSSTGYPEPQ 11  
 ||:|||||  
 DB 164 CTSAGWPEPQ 174

## RESULT 12

A37821  
 butyrophilin - bovine  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 30-Apr-1991 #sequence\_revision 30-Apr-1991 #text\_change 09-Jul-2004  
 C/Accession: A37821  
 R/Jack, L.J.W.; Mather, I.H.  
 J. Biol. Chem. 265, 14481-14486, 1990  
 A/Title: Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycoprot

A/Reference number: A37821; MUID:90354441; PMID:2387867  
 A/Accession: A37821  
 A/Status: preliminary  
 A/Molecule type: mRNA

A:Residues: 1-526 <JAC>  
 A:Cross-references: UNIPROT:P18692; GB:M35551; NID:G1763665; PIDN:AAB39766.1; PID:G16277  
 C:Superfamily: rfp transforming protein  
 C:Keywords: transmembrane protein

Query Match 59.4%; Score 41; DB 2; Length 526;  
 Best Local Similarity 63.6%; Pred. No. 32;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSSTGQYPEPQ 11  
 ||:|||||  
 DB 164 CTSVGMYPPEQ 174

RESULT 13

T29549  
 hypothetical protein ZK377.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C:Accession: T29549

R:Nhan, M.; Hawkins, J.

A:Description: The sequence of C. elegans cosmid ZK377.

A:Reference number: Z20639

A:Accession: T29549

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-423 <NHA>

A:Cross-references: EMBL:U88183; PIDN:AAB52658.1; GSPDB:GN00028; CESP:ZK377.3

C:Genetics:

A:Gene: CESP:ZK377.3

A:Map position: X

A:introns: 24/1; 142/3; 229/3; 284/2; 408/3

Query Match 58.0%; Score 40; DB 2; Length 423;  
 Best Local Similarity 60.0%; Pred. No. 38;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGQYPEP 10  
 ||:|||||  
 DB 153 CSPPRGFPPEP 162

RESULT 14

T42405  
 sax-3 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: T42405

R:Zallen, J.A.; Yi, B.A.; Bargmann, C.I.

Cell 92, 217-227, 1998

A:Title: The conserved immunoglobulin superfamily member SAX-3/Robo directs multiple asp

A:Reference number: Z22160; MUID:98117250; PMID:9458046

A:Accession: T42405

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1273 <ZAL>

A:Cross-references: UNIPROT:O44928; EMBL:AF041053; NID:G2804779; PIDN:AAC38848.1; PID:92

C:Genetics:

A:Note: sax-3

C:Function:

A:Description: sax-3 function is required at the time of axon guidance

Query Match 58.0%; Score 40; DB 2; Length 1273;  
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGQYPEP 10  
 ||:|||||  
 DB 154 CSPPRGFPPEP 163

RESULT 15

C48150  
 hibernation-related protein HP-27 precursor - Siberian chipmunk

C:Species: Eutamias sibiricus (Siberian chipmunk)

C:Date: 16-Feb-1994 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C:Accession: C48150; A41752

R:Takanatsu, N.; Ohba, K.; Kondo, U.; Kondo, N.; Shiba, T.

Mol. Cell. Biol. 13, 1516-1521, 1993

A:Title: Hibernation-associated gene regulation of plasma proteins with a collagen-like

A:Reference number: A48150; MUID:93180798; PMID:8441393

A:Accession: C48150

A:Molecule type: mRNA; protein

A:Residues: 1-215 <TAK>

A:Cross-references: UNIPROT:O06577; GB:D12976; NID:G287471; PIDN:BA02353.1; PID:G28747

A:Note: the source is designated as Tamias asiaticus in Genbank entry TMSHP27, release

A:Note: sequence extracted from NCBI backbone (NCBIN:125948, NCBI:P:125949)

R:Kondo, N.; Kondo, U.

U. Biol. Chem. 267, 473-478, 1992

A:Title: Identification of novel blood proteins specific for mammalian hibernation.

A:Reference number: A41752; MUID:92112696; PMID:1730610

A:Accession: A41752

A:Status: preliminary

A:Molecule type: protein

A:Residues: 31-40, 'A', 42-50, 'Q', 52-215 <KON>

C:Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal hot

C:Keywords: glycoprotein; hibernation; plasma

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-215/Product: hibernation-related protein HP-27 #status experimental <NAT>

F:31-214/Domain: complement C1q carboxyl-terminal homology <CIQ>

F:155/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.5%; Score 39; DB 2; Length 215;  
 Best Local Similarity 77.8%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGQYPE 9  
 ||:|||||  
 DB 29 CSSTGQNP 37

..

Search completed: December 15, 2004, 16:38:02  
 Job time: 16.2857 sec

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:24:31 / Search time 66.2857 Seconds  
(without alignments)

104.163 Million cell updates/sec

Title: US-09-868-605-14\_COPY\_151\_162

Sequence: 1 CSSTGCGYPEPOR 12

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match Length | ID               | Description         |
|------------|-------|--------------------|------------------|---------------------|
| 1          | 69    | 100.0              | 325 2 002838     | 002838 sus scrofa   |
| 2          | 63    | 91.3               | 284 2 09GLJ3     | 09GLJ3 bos taurus   |
| 3          | 57    | 82.6               | 330 1 CD86.RABIT | P42071 coryctolagus |
| 4          | 54    | 78.3               | 280 2 09TTF1     | 09TTF1 canis fami   |
| 5          | 54    | 78.3               | 329 2 09TTF2     | 09TTF2 canis fami   |
| 6          | 54    | 78.3               | 329 2 09XSK6     | 09XSK6 felis silve  |
| 7          | 54    | 78.3               | 332 2 09GMW7     | 09GMW7 felis silve  |
| 8          | 54    | 78.3               | 332 2 09SLI6     | 09SLI6 felis silve  |
| 9          | 52    | 75.4               | 275 2 09BDN9     | 09BDN9 papio anubi  |
| 10         | 52    | 75.4               | 323 2 09BDN8     | 09BDN8 cercopithec  |
| 11         | 52    | 75.4               | 323 2 09BDK2     | 09BDK2 cercopithec  |
| 12         | 52    | 75.4               | 323 2 09BDK4     | 09BDK4 macaca mula  |
| 13         | 52    | 75.4               | 323 2 09BDW9     | 09BDW9 macaca neme  |
| 14         | 51    | 73.9               | 329 1 CD86.HUMAN | P42081 homo sapien  |
| 15         | 51    | 73.9               | 329 2 AAH40261   | AAH40261 homo sapi  |
| 16         | 50    | 72.5               | 149 2 062810     | 062810 rattus norv  |
| 17         | 50    | 72.5               | 313 2 035531     | 035531 rattus norv  |
| 18         | 47    | 68.1               | 313 2 08CJ58     | 08CJ58 mesocricetu  |
| 19         | 46    | 66.7               | 316 2 06UX12     | 06UX12 homo sapien  |
| 20         | 46    | 66.7               | 316 2 07TPB4     | 07TPB4 rattus norv  |
| 21         | 46    | 66.7               | 316 2 08VE98     | 08VE98 mus musculu  |
| 22         | 46    | 66.7               | 316 2 AAH56608   | AAH56608 mus muscu  |
| 23         | 46    | 66.7               | 316 2 AAQ88709   | AAQ88709 homo sapi  |
| 24         | 46    | 66.7               | 388 2 08NC34     | 08NC34 homo sapien  |
| 25         | 46    | 66.7               | 493 2 06PSY4     | 06PSY4 homo sapien  |
| 26         | 46    | 66.7               | 493 2 AAH62581   | AAH62581 homo sapi  |
| 27         | 46    | 66.7               | 533 2 08NCB6     | 08NCB6 homo sapien  |
| 28         | 44    | 63.8               | 309 1 08NCB8     | 08NCB8 homo sapien  |
| 29         | 44    | 63.8               | 309 1 CD86.MOUSE | P42082 mus musculu  |
| 30         | 44    | 63.8               | 309 1 AAD25880   | AA25880 mus muscu   |
| 31         | 44    | 63.8               | 309 2 AAD25881   | AA25881 mus muscu   |

## ALIGNMENTS

| RESULT 1              | ID                                                                    | PRELIMINARY                             | PRT | 325 AA  | ALIGNMENTS |
|-----------------------|-----------------------------------------------------------------------|-----------------------------------------|-----|---------|------------|
| 002838                | AC                                                                    | 002838                                  |     |         |            |
| DT                    | 01-JUL-1997                                                           | (TREMBLrel. 04, Created)                |     |         |            |
| DT                    | 01-JUL-1997                                                           | (TREMBLrel. 04, Last sequence update)   |     |         |            |
| DT                    | 01-OCT-2003                                                           | (TREMBLrel. 25, Last annotation update) |     |         |            |
| DE                    | B7-2.                                                                 |                                         |     |         |            |
| GN                    | Name=CD86;                                                            |                                         |     |         |            |
| OS                    | Sus scrofa (Pig).                                                     |                                         |     |         |            |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |                                         |     |         |            |
| OC                    | Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.              |                                         |     |         |            |
| OX                    | NCBI_TaxID=9823;                                                      |                                         |     |         |            |
| RN                    | [1]                                                                   |                                         |     |         |            |
| RP                    | SEQUENCE FROM N.A.                                                    |                                         |     |         |            |
| RX                    | MEDLINE=97047772; PubMed=8892613;                                     |                                         |     |         |            |
| RA                    | Maier S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,              |                                         |     |         |            |
| RA                    | Bothwell A.L.;                                                        |                                         |     |         |            |
| RT                    | "Porcine endothelial CD86 is a major costimulator of xenogeneic human |                                         |     |         |            |
| RT                    | T cells: cloning, sequencing, and functional expression in human      |                                         |     |         |            |
| RT                    | endothelial cells";                                                   |                                         |     |         |            |
| RL                    | J. Immunol. 157:3838-3844(1996).                                      |                                         |     |         |            |
| DR                    | EMBL; L76099; AAB61307.1; -.                                          |                                         |     |         |            |
| DR                    | HSSP; P42081; INCN.                                                   |                                         |     |         |            |
| DR                    | InterPro; IPR007110; IG-1like.                                        |                                         |     |         |            |
| DR                    | InterPro; IPR003596; IG_V.                                            |                                         |     |         |            |
| DR                    | Pfam; PF00047; IG_1.                                                  |                                         |     |         |            |
| DR                    | SMART; SM00406; IG_1.                                                 |                                         |     |         |            |
| DR                    | PROSITE; PS00835; IG_LIKE; 1.                                         |                                         |     |         |            |
| SO                    | SEQUENCE 325 AA; 36527 MW; 988BE08137B0597D CRC64;                    |                                         |     |         |            |
| Query Match           | 100.0%; Score 69; DB 2; Length 325;                                   |                                         |     |         |            |
| Best local similarity | 100.0%; Pred. No. 0.00076;                                            |                                         |     |         |            |
| Matches               | 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                   |                                         |     |         |            |
| QY                    | 1 CSSTGCGYPEPOR 12                                                    |                                         |     |         |            |
| DB                    | 151 CSSTGCGYPEPOR 162                                                 |                                         |     |         |            |
| RESULT 2              |                                                                       |                                         |     |         |            |
| Q9GLJ3                |                                                                       |                                         |     |         |            |
| ID                    | Q9GLJ3                                                                | PRELIMINARY                             | PRT | 284 AA. |            |
| AC                    | Q9GLJ3                                                                |                                         |     |         |            |
| DT                    | 01-MAR-2001                                                           | (TREMBLrel. 16, Created)                |     |         |            |
| DT                    | 01-MAR-2001                                                           | (TREMBLrel. 16, Last sequence update)   |     |         |            |
| DT                    | 01-OCT-2003                                                           | (TREMBLrel. 25, Last annotation update) |     |         |            |
| DE                    | CD86 antigen (Fragment).                                              |                                         |     |         |            |
| GN                    | Name=CD86;                                                            |                                         |     |         |            |
| OS                    | Bos taurus (Bovine).                                                  |                                         |     |         |            |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |                                         |     |         |            |
| OC                    | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;     |                                         |     |         |            |
| OC                    | Bovinae; Bos.                                                         |                                         |     |         |            |
| OX                    | NCBI_TaxID=9913;                                                      |                                         |     |         |            |

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Brooke G.P., Howard C.J., Parsons K.R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; A0291475; CAC13140.1; -.
DR InterPro; IPR007110; IG-1-like.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 284 AA; 284 AA; 1.
SQ SEQUENCE 284 AA; 32021 MW; 797B8639B297841 CRC64;

Query Match
Best Local Similarity 91.3%; Score 63; DB 2; Length 284;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTOQYPPRQ 12
DB 165 CSSTOQYPPRQ 176

RESULT 3
CD86 RABIT STANDARD; PRT; 330 AA.
AC P42071;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE B lymphocyte activation antigen CD86 precursor (Activation B7-2
  antigen)
GN Name=CD86;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B/O X CHBR;HM;
RA MEDLINE=95369849; PubMed=7642234;
RX Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
  costimulatory molecules."
RL Immunogenetics 42:217-220(1995).
CC -!- FUNCTION: Receptor involved in the costimulatory signal essential
  for T lymphocyte proliferation and interleukin 2 production, by
  binding CD28 or CTLA-4. May play a critical role in the early
  events of T cell activation and costimulation of native T cells,
  such as deciding between immunity and anergy that is made by T
  cells within 24 hours after activation.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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  CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D49842; BAA08642.1; -.
DR PIR; I4691; I4691.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Immunoglobulin domain; Receptor; signal; T-cell;

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KW Transmembrane.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 330 B lymphocyte activation antigen CD86.
FT DOMAIN 23 247 Extracellular (Potential).
FT TRANSMEM 248 268 Potential.
FT DOMAIN 269 330 Cytoplasmic (Potential).
FT DOMAIN 33 337 Ig-like V-type.
FT DOMAIN 150 225 Ig-like C2-type.
FT DISULFID 40 110 Potential.
FT DISULFID 157 218 Potential.
FT CARBOHYD 133 333 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 146 146 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 154 154 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 177 177 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 192 192 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 198 198 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 213 213 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 330 AA; 37142 MW; 935CDB5C57E3EE1 CRC64;

Query Match
Best Local Similarity 82.6%; Score 57; DB 1; Length 330;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTOQYPPRQ 12
DB 157 CSSTOQYPPRQ 168

RESULT 4
O9TTF1 PRELIMINARY; PRT; 280 AA.
AC O9TTF1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE Truncated B7-2 protein.
GN Name=CD86;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20093996; PubMed=10630300;
RX Yang S., Sim G.-K.;
RT "New forms of dog CD80 and CD86 transcripts that encode secreted B7
  molecules."
RL Immunogenetics 50:349-353(1999).
DR EMBL; AF106827; AAF17298.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKOWN 1.
SQ SEQUENCE 280 AA; 32265 MW; 3C8BCA4D826A7F3 CRC64;

Query Match
Best Local Similarity 78.3%; Score 54; DB 2; Length 280;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTOQYPPRQ 11
DB 158 CSSTOQYPPRQ 168

RESULT 5
O9TTF2 PRELIMINARY; PRT; 329 AA.
AC O9TTF2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, last annotation update)
DE B7-2 protein.
GN Name=CD86;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20033996; Pubmed=10630300;
RA Yang S., Sim G.-K.;
RT "New forms of dog CD80 and CD86 transcripts that encode secreted B7
RT molecules.";
RL Immunogenetics 50:349-353(1999).
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003506; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 329 AA; 37774 MW; D95BB63437BF7B73 CRC64;

Query Match 78.3%; Score 54; DB 2; Length 329;
Best Local Similarity 81.8%; Pred. No. 0.37;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11
DB 158 CSSTQGYPEPK 168

RESULT 6
Q9XSX6 PRELIMINARY; PRT; 329 AA.
ID Q9XSX6
AC Q9XSX6;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE CD86 antigen.
GN Name=CD86;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20180222; Pubmed=10713336;
RA Choi I.-S., Hash S.M., Winslow B.J., Collisson E.W.;
RT "Sequence analyses of feline B7 costimulatory molecules.";
RL Vet. Immunol. Immunopathol. 73:219-231(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Choi I.-S., Hash S., Winslow B.J., Collisson E.W.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157827; AAD42974.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 329 AA; 37481 MW; A10621E3C00A08BB CRC64;

Query Match 78.3%; Score 54; DB 2; Length 329;
Best Local Similarity 81.8%; Pred. No. 0.37;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11
DB 159 CSSTQGYPEPK 169

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RESULT 7
Q9GMZ7 PRELIMINARY; PRT; 332 AA.
ID Q9GMZ7
AC Q9GMZ7;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE B-lymphocyte activation antigen B7-2 (CD86).
GN Name=CD86;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20485322; Pubmed=11029611;
RA Nishimura Y., Shimojima M., Miyazawa T., Sato E., Nakamura K.,
RA Izumiya Y., Ikeda Y., Mikami T., Takahashi E.;
RT "Molecular cloning of the cDNA encoding the feline B-lymphocyte
RT activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which
RT interact with human CTLA-4-1g.";
RL Eur. J. Immunogenet. 27:427-430(2000).
DR EMBL; AB030652; BAB11688.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 332 AA; 37812 MW; 672C8B3667D1E3C0 CRC64;

Query Match 78.3%; Score 54; DB 2; Length 332;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11
DB 159 CSSTQGYPEPK 169

RESULT 8
Q9SLI6 PRELIMINARY; PRT; 332 AA.
ID Q9SLI6
AC Q9SLI6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE CD86.
GN Name=CD86;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21390213; Pubmed=11498243;
RA Yang S., Sellins K.S., Powell T., Stoneman E., Sim G.-K.;
RT "Novel transcripts encoding secreted forms of feline CD80 and CD86
RT costimulatory molecules.";
RL Vet. Immunol. Immunopathol. 81:15-21(2001).
DR EMBL; AY007704; AAG23342.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 332 AA; 37826 MW; 9BFC8B3667D1E3D8 CRC64;

Query Match 78.3%; Score 54; DB 2; Length 332;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11

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Db 159 CSSTGYPEPCK 169

## RESULT 9

ID Q9BDN9 PRELIMINARY; PRT; 275 AA.

AC Q9BDN9; 01-JUN-2001 (TRMBLrel. 17, Created)  
 DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)  
 DE CD86 protein precursor.  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecidae; Papio.  
 NCBI\_TaxID=9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=21383618; PubMed=11491535;  
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,  
 Weiss W.R., Ansari A.A.;  
 RT "Cloning, sequencing, and homology analysis of nonhuman primate  
 Fas/Fas-ligand and co-stimulatory molecules.";  
 RL Immunogenetics 53:315-328(2001).  
 DR EMBL; AF344836; AAK37532.1; -.  
 DR HSSP; P42081; INCN.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; IG\_V.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Signal.  
 FT SIGNAL. 1 17 Potential.  
 SQ SEQUENCE 275 AA; 31343 MW; 3AAND3481B4F37C19 CRC64;

Query Match 75.4%; Score 52; DB 2; Length 275;  
 Best Local Similarity 66.7%; Pred. No. 0.69;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPCK 12  
 Db 151 CSSTGYPEPCK 162

RESULT 10  
 ID Q9BDN8 PRELIMINARY; PRT; 323 AA.  
 AC Q9BDN8; 01-JUN-2001 (TRMBLrel. 17, Created)  
 DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)  
 DE CD86 protein precursor.  
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecidae; Cercopithecus.  
 NCBI\_TaxID=9531;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21383618; PubMed=11491535;  
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,  
 Weiss W.R., Ansari A.A.;  
 RT "Cloning, sequencing, and homology analysis of nonhuman primate  
 Fas/Fas-ligand and co-stimulatory molecules.";  
 RL Immunogenetics 53:315-328(2001).  
 DR EMBL; AF344840; AAK37536.1; -.  
 DR HSSP; P42081; INCN.  
 DR GO; GO:0016021; C:integral to membrane; ISS.  
 DR GO; GO:0005026; F:coreceptor activity; ISS.  
 DR GO; GO:0005515; F:protein binding; ISS.  
 DR GO; GO:0016563; F:transcriptional activator activity; ISS.  
 DR GO; GO:0007267; P:cell-cell signaling; ISS.  
 DR GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.

DR GO; GO:004504; P:positive regulation of interleukin-4 biosyn. . .; ISS.  
 DR GO; GO:0045630; P:positive regulation of T-helper 2 cell diff. . .; ISS.  
 DR GO; GO:0045941; P:positive regulation of transcription; ISS.  
 DR GO; GO:0043017; P:positive regulation of tumor necrosis facto. . .; ISS.  
 DR GO; GO:0042110; P:T-cell activation; ISS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; IG\_V.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Signal.  
 FT SIGNAL. 17 323 Potential.  
 FT CHAIN. 17 323 CD86 protein.  
 SQ SEQUENCE 323 AA; 37010 MW; 45B217660A79B75 CRC64;

Query Match 75.4%; Score 52; DB 2; Length 323;  
 Best Local Similarity 66.7%; Pred. No. 0.83;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPCK 12  
 Db 151 CSSTGYPEPCK 162

RESULT 11  
 ID Q9BDM2 PRELIMINARY; PRT; 323 AA.  
 AC Q9BDM2; 01-JUN-2001 (TRMBLrel. 17, Created)  
 DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)  
 DE CD86 protein.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecidae; Cercopithecus.  
 NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21383618; PubMed=11491535;  
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,  
 Weiss W.R., Ansari A.A.;  
 RT "Cloning, sequencing, and homology analysis of nonhuman primate  
 Fas/Fas-ligand and co-stimulatory molecules.";  
 RL Immunogenetics 53:315-328(2001).  
 DR EMBL; AF344861; AAK37543.1; -.  
 DR HSSP; P42081; INCN.  
 DR GO; GO:0016021; C:integral to membrane; ISS.  
 DR GO; GO:0015026; F:coreceptor activity; ISS.  
 DR GO; GO:0005515; F:protein binding; ISS.  
 DR GO; GO:0016563; F:transcriptional activator activity; ISS.  
 DR GO; GO:0007267; P:cell-cell signaling; ISS.  
 DR GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.  
 DR GO; GO:0045404; P:positive regulation of interleukin-4 biosyn. . .; ISS.  
 DR GO; GO:0045630; P:positive regulation of T-helper 2 cell diff. . .; ISS.  
 DR GO; GO:0045941; P:positive regulation of transcription; ISS.  
 DR GO; GO:0043017; P:positive regulation of tumor necrosis facto. . .; ISS.  
 DR GO; GO:0042110; P:T-cell activation; ISS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; IG\_V.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 SQ SEQUENCE 323 AA; 37045 MW; 3E43152A8ED17267 CRC64;

Query Match 75.4%; Score 52; DB 2; Length 323;  
 Best Local Similarity 66.7%; Pred. No. 0.83;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPCK 12  
 Db 151 CSSTGYPEPCK 162

## RESULT 12



```

Q9BDM4 PRELIMINARY; PRT; 323 AA.
ID Q9BDM4
AC Q9BDM4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CD86 protein precursor.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
NCBI_TaxID=9544;
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344857; AAK37540.1; -.
DR HSSP; P42081; INCN.
DR GO; GO:0016021; C:integral to membrane; ISS.
DR GO; GO:0015026; F:coreceptor activity; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0016563; F:transcriptional activator activity; ISS.
DR GO; GO:0007267; P:cell-cell signaling; ISS.
DR GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
DR GO; GO:0045404; P:positive regulation of interleukin-4 biosyn. . .; ISS.
DR GO; GO:0045630; P:positive regulation of T-helper 2 cell diff. . .; ISS.
DR GO; GO:0045941; P:positive regulation of transcription; ISS.
DR GO; GO:0043017; P:positive regulation of tumor necrosis facto. . .; ISS.
DR GO; GO:0042107; P:T-cell activation; ISS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
KM SIGNAL.
FT SIGNAL.
SQ SEQUENCE 323 AA; 37019 MW; D211D103DB1A7D7A CRC64;

Query Match 75.4%; Score 52; DB 2; Length 323;
Best Local Similarity 66.7%; Pred. No. 0.83;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPOR 12
DB 151 CSSTHGYPEPEPK 162

RESULT 13
Q9BDM9 PRELIMINARY; PRT; 323 AA.
ID Q9BDM9
AC Q9BDM9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CD86 protein precursor.
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
NCBI_TaxID=9545;
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344851; AAK37611.1; -.
DR HSSP; P42081; INCN.

QY 1 CSSTQGYPEPOR 12
DB 151 CSSTHGYPEPEPK 162

RESULT 14
CD86_HUMAN STANDARD; PRT; 329 AA.
ID CD86_HUMAN
AC P42081; Q13655; Q7M4L5;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE T lymphocyte activation antigen CD86 precursor (Activation B7-2
DE antigen) (CTLA-4 counter-receptor B7.2) (B70) (B053).
GN Name=CD86; Synonyms=CD28LG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=94053735; PubMed=7694363;
RA Freeman G.J., Gribben J.G., Boussiotis V.A., Ng J.W.,
RA Restivo V.A., Jr., Lombard L.A., Gray G.S., Nadler L.M.;
RT "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T
RT cell proliferation.";
RL Science 262:909-911(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=21092744; PubMed=11162656; DOI=10.1006/birc.2000.4102;
RA Magistrelli G., Caron G., Gauchat J.F., Jeannin P., Bonnefoy Y.,
RA Delneste Y.;
RT "Identification of an alternatively spliced variant of human CD86
RL mRNA.";
RL Biochem. Biophys. Res. Commun. 280:1211-1215(2001).
RN [3]
RP SEQUENCE OF 7-329 FROM N.A. (ISOFORM 1).
RX MEDLINE=94050123; PubMed=7694153;
RA Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H., Lanier L.L.,
RA Somiya C.;
RT "B70 antigen is a second ligand for CTLA-4 and CD28.";
RL Nature 366:76-79(1993).
RN [4]
RP SEQUENCE OF 7-329 FROM N.A. (ISOFORM 1).
RX TISSUE=ForeSkin;
RL MEDLINE=95331831; PubMed=7541777;
RA Tellis C.L., Wang S.S., Renner P., Borriello F., Sharpe A.H.,
RA Green N.R., Gray G.S.;
RT "Genomic organization of the gene coding for the costimulatory human
RT B-lymphocyte antigen B7-2 (CD86).";

```

Immunogenetics 42:85-89(1995).

RL [5]

RN CHARACTERIZATION.

RX MEDLINE=95088403; PubMed=7527824;

RA Ianier L.L., O'Fallon S., Somosa C., Phillips J.H., Linsley P.S.,

RT Okumura K., Ito D., Azuma M.,

RT CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T

cell proliferation, cytokine production, and generation of CTLs.

RL J. Immunol. 154:97-105(1995).

RP IDENTIFICATION AS CD86.

RX MEDLINE=94348060; PubMed=7520767;

RA Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,

RT Nadler L.M., Wakasa H., Tedder T.F.,

RT "The B7-2 (B70) costimulatory molecule expressed by monocytes and

activated B lymphocytes is the CD86 differentiation antigen."

RL Blood 84:1402-1407(1994).

CC - FUNCTION: Receptor involved in the costimulatory signal essential

for T lymphocyte proliferation and interleukin 2 production. By

binding CD28 or CTLA-4. May play a critical role in the early

events of T cell activation and costimulation of naive T cells,

such as deciding between immunity and anergy that is made by T

cells within 24 hours after activation. Isoform 2 interferes with

the formation of CD86 clusters, and thus acts as a negative

regulator of T cell activation.

CC - SUBCELLULAR LOCATION: Type I membrane protein.

CC - ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=PA2081-1; Sequence=Displayed;

CC Name=2; Synonyms=CD86 deltaEC;

CC IsoId=PA2081-2; Sequence=VSP 009125;

CC - TISSUE SPECIFICITY: Expressed by activated B lymphocytes and

monocytes.

CC - SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC - SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC - DATABASE: NAME=PROV; NOTE=CD guide CD86 entry;

CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd86.htm".

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

DR EMBL, L25259; AAAS8389.1; -

DR EMBL, U04343; AAB03814.1; -

DR EMBL, U17722; AA86473.1; -

DR EMBL, U17717; AA86473.1; JOINED.

DR EMBL, U17718; AA86473.1; JOINED.

DR EMBL, U17719; AA86473.1; JOINED.

DR EMBL, U17721; AA86473.1; JOINED.

DR FIR, A48754; A48754.

DR FIR, JCT605; JCT605.

DR PDB, 1I85; X-ray; A/B=25-134.

DR PDB, INCN; X-ray; A/B=25-134.

DR Genew; HGNC:1705; CD86.

DR MIM: 601020; -

DR GO, GO:0016021; C: integral to membrane; IC.

DR GO, GO:0015026; F: coreceptor activity; NAS.

DR GO, GO:0005515; F: protein binding; IPI.

DR GO, GO:0016563; F: transcriptional activator activity; NAS.

DR GO, GO:0007267; P: cell-cell signaling; IC.

DR GO, GO:0006955; P: immune response; TNS.

DR GO, GO:0006284; P: positive regulation of cell proliferation; TNS.

DR GO, GO:0045086; P: positive regulation of interleukin-2 biosyn. . . ; NAS.

DR GO, GO:0045404; P: positive regulation of interleukin-4 biosyn. . . ; NAS.

DR GO, GO:0045630; P: positive regulation of T-helper 2 cell diff. . . ; NAS.

DR GO, GO:0045941; P: positive regulation of transcription; NAS.

DR GO, GO:0043017; P: positive regulation of tumor necrosis facto. . . ; NAS.

DR GO, GO:0042110; P: T-cell activation; IC.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003006; IG MHC.

DR PROSITE: PSS0835; IG\_LIKE; 1.

DR PROSITE: PSS0290; IG\_MHC; FALSE\_NEG.

KW 3D-structure; Alternative splicing; Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Signal; T-cell; Transmembrane.

KW Transmembrane.

FT SIGNAL 1 23

FT CHAIN 24 329

FT DOMAIN 24 247

FT TRANSMEM 248 268

FT DOMAIN 269 329

FT DOMAIN 33 131

FT DOMAIN 150 225

FT DISULFID 40 110

FT DISULFID 157 218

FT CARBOHYD 33 33

FT CARBOHYD 47 47

FT CARBOHYD 135 135

FT CARBOHYD 146 146

FT CARBOHYD 154 154

FT CARBOHYD 177 177

FT CARBOHYD 192 192

FT CARBOHYD 213 213

FT VARSPLIC 22 234

FT VARIANT 310 310

FT CONFLICT 27 27

FT STRAND 27 31

FT TURN 32 33

FT STRAND 36 37

FT TURN 50 51

FT STRAND 54 58

FT TURN 60 61

FT STRAND 64 69

FT TURN 70 71

FT STRAND 72 73

FT TURN 76 77

FT TURN 80 84

FT STRAND 86 89

FT TURN 90 93

FT STRAND 94 97

FT STRAND 107 113

FT STRAND 122 133

SO SEQUENCE 329 AA; 37696 MW; 65D4F3826889CF7D CRC64;

Query Match 73.9%; Score 51; DB 1; Length 329;

Best Local Similarity 66.7%; Pred. No. 1.3;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPPEPQR 12

Db 157 CSIHGYPEPKK 168

RESULT 15

AAH40261 PRELIMINARY; PRT; 329 AA.

AC AAH40261;

DT 02-VAR-2004 (TREMBLrel. 27, Created)

DT 02-VAR-2004 (TREMBLrel. 27, Last sequence update)

DT 02-VAR-2004 (TREMBLrel. 27, Last annotation update)

DS CD86 antigen, isoform 1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primata; Catarrhini; Hominiidae; Homo.

OX NCBI\_TaxID=9606;

RN (1) \_

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.C.,



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CC human T cells, with particular importance in the context of  
 CC xenotransplantation of porcine organs. Recipients are immunised with  
 CC hybrid synthetic peptides comprising a T cell epitope conjugated to  
 CC sequences of the porcine costimulatory molecules CD80, CD86 or CD40 (see  
 CC AAY95321-24). Peptides that induce antibodies specific for regions of  
 CC costimulatory molecules involved in binding to their counter-receptors on  
 CC human cells (CD28 and CD14) are capable of blocking the delivery of  
 CC costimulation. Once the antibody response has been induced, the  
 CC transplanted organ will recall this response due to the expression of the  
 CC costimulatory molecules, thereby sustaining the response, and providing  
 CC an endogenous mechanism of costimulatory blockade. The method is useful  
 CC for improving the tolerance of a host to xenografts, particularly porcine  
 CC pancreatic islet cells

XX  
 SQ Sequence 325 AA;

Query Match 98.5%; Score 325; DB 3; Length 325;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-306;  
 Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSNILFVWVLLSGAASLSKQAYFNETGELPCHFTNSQNLSDLELVIWQDDNLVLY 60  
 DB 1 MGLSNILFVWVLLSGAASLSKQAYFNETGELPCHFTNSQNLSDLELVIWQDDNLVLY 60  
 QY 61 ELYRQGEKPHNVNSKVMGRISFDQATWTLRLAHNVQIKDKGSYOCFIHHKGGHGLVPIHOM 120  
 DB 61 ELYRQGEKPHNVNSKVMGRISFDQATWTLRLAHNVQIKDKGSYOCFIHHKGGHGLVPIHOM 120  
 QY 121 SSDLSLVANFQPEINILNHTENSVINLTCSSIOGYPEPQRMWMLNTKNSSTTEHDADM 180  
 DB 121 SSDLSLVANFQPEINILNHTENSVINLTCSSIOGYPEPQRMWMLNTKNSSTTEHDADM 180  
 QY 181 KKSQNNITELYNVNSIRVSLPIPETNVSIVCVQLQEPKTLFLSPCNIDAKPPVQPPVP 240  
 DB 181 KKSQNNITELYNVNSIRVSLPIPETNVSIVCVQLQEPKTLFLSPCNIDAKPPVQPPVP 240  
 QY 241 DHILMIALLVTVVVCGWVSFVTLRKRKKQPGPSNECGETIKMRKASEQTNRAREVH 300  
 DB 241 DHILMIALLVTVVVCGWVSFVTLRKRKKQPGPSNECGETIKMRKASEQTNRAREVH 300  
 QY 301 ERSDDAQCDVNIILKTASDNDSTTDF 325  
 DB 301 ERSDDAQCDVNIILKTASDNDSTTDF 325

RESULT 2  
 AAY95321

XX ID AAY95321 standard; protein; 325 AA.

XX AC AAY95321;

XX DT 25-SEP-2000 (first entry)

XX DE Pig costimulatory molecule CD86 (B7-2).

XX KW Co-stimulatory molecule; CD86, B7-2; pig; immunosuppressive;  
 KW xenotransplantation; organ transplant; vaccine; epitope.

XX OS Sus scrofa.

XX XX Location/Qualifiers

XX FH Peptide 17..29

XX FT Peptide 21..32 "peptide 9"

XX FT Peptide 32..40 "peptide 8"

XX FT Peptide 40..48 "peptide 2"

XX FT Peptide 48..56 "peptide 10"

XX FT Peptide 56..64 "peptide 1"

XX FT Peptide 64..72 "peptide 5"

FT Peptide 109..121  
 FT /note="peptide 3"  
 FT Peptide 113..121  
 FT /note="peptide 4"  
 FT Peptide 151..162  
 FT /note="peptide 6"

FN WO200037102-A2.

XX 29-JUN-2000.

PP 17-DEC-1999; 99WO-GB004200.

XX 19-DEC-1998; 98GB-00027921.

PR 23-OCT-1999; 99GB-00025015.

XX (MIMU-) ML LAB PLC.

PI Lechner RI, Rogers NJ, Dorling A;

DR WPI; 2000-442537/38.

XX N-PSDB; AAA49661.

PS Disclosure; Fig 6; 81pp; English.

The present sequence is that of pig co-stimulatory molecule CD86 (B7-2),  
 as deduced from an isolated cDNA clone (see AAA49661). CD86 plays a key  
 role in T cell costimulation. The invention relates to a novel strategy  
 for inhibiting costimulation by porcine cells of human T cells, with  
 particular importance in the context of xenotransplantation of porcine  
 organs. Recipients are immunised with hybrid synthetic peptides  
 comprising a T cell epitope conjugated to sequences of the porcine  
 costimulatory molecules CD80, CD86 or CD40, such as peptides 1-10 of CD86  
 (see also AAY95325-33). Peptides that induce antibodies specific for  
 regions of costimulatory molecules involved in binding to their counter-  
 receptors on human cells (CD28 and CD14) are capable of blocking the  
 delivery of costimulation. Once the antibody response has been induced,  
 the transplanted organ will recall this response due to the expression of  
 the costimulatory molecules, thereby sustaining the response, and  
 providing an endogenous mechanism of costimulatory blockade. The method  
 is useful for improving the tolerance of a host to xenografts,  
 particularly porcine pancreatic islet cells

SQ Sequence 325 AA;

Query Match 67.9%; Score 224; DB 3; Length 325;  
 Best Local Similarity 99.7%; Pred. No. 2.9e-208;  
 Matches 324; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGLSNILFVWVLLSGAASLSKQAYFNETGELPCHFTNSQNLSDLELVIWQDDNLVLY 60  
 DB 1 MGLSNILFVWVLLSGAASLSKQAYFNETGELPCHFTNSQNLSDLELVIWQDDNLVLY 60  
 QY 61 ELYRQGEKPHNVNSKVMGRISFDQATWTLRLAHNVQIKDKGSYOCFIHHKGGHGLVPIHOM 120  
 DB 61 ELYRQGEKPHNVNSKVMGRISFDQATWTLRLAHNVQIKDKGSYOCFIHHKGGHGLVPIHOM 120  
 QY 121 SSDLSLVANFQPEINILNHTENSVINLTCSSIOGYPEPQRMWMLNTKNSSTTEHDADM 180  
 DB 121 SSDLSLVANFQPEINILNHTENSVINLTCSSIOGYPEPQRMWMLNTKNSSTTEHDADM 180  
 QY 181 KKSQNNITELYNVNSIRVSLPIPETNVSIVCVQLQEPKTLFLSPCNIDAKPPVQPPVP 240  
 DB 181 KKSQNNITELYNVNSIRVSLPIPETNVSIVCVQLQEPKTLFLSPCNIDAKPPVQPPVP 240  
 QY 241 DHILMIALLVTVVVCGWVSFVTLRKRKKQPGPSNECGETIKMRKASEQTNRAREVH 300  
 DB 241 DHILMIALLVTVVVCGWVSFVTLRKRKKQPGPSNECGETIKMRKASEQTNRAREVH 300  
 QY 301 ERSDDAQCDVNIILKTASDNDSTTDF 325

Db 301 ERSDDACQCVNIIKTASDNDSTTDF 325

RESULT 3  
ID AAM14944 standard; protein; 250 AA.  
AC AAM14944;

DT 17-OCT-2003 (revised)  
DT 16-JUN-1997 (first entry)  
XX Chimeric human/porcine CD86.  
XX Xenotransplantation; graft rejection; cell interaction; pig; CD86;  
XX monoclonal antibody; chimeric antibody; diagnosis.  
XX Homo; sapiens.  
XX Sus scrofa.  
XX Chimeric.

PH Key Location/Qualifiers  
FT Peptide 1..25  
FT Protein /label= Sig\_peptide  
FT Protein /label= Mac\_protein  
FT Region 246..250  
FT /label= Histidine\_tag

XX WO9711971-A1.  
XX 03-APR-1997.  
XX 27-SEP-1996; 96WO-US015575.  
XX 28-SEP-1995; 95US-0004489P.  
XX 26-SEP-1996; 96US-00004489.  
XX (ALEX-) ALEXION PHARM INC.

PI Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Mattis LA;  
DR WPI; 1997-212855/19.  
DR N-PSDB; AAT62939.  
XX Antibodies binding to porcine but not human cell interaction proteins -  
PT useful to treat and assay for rejection of xenografted porcine organs,  
PT tissues or cells.  
XX Disclosure; Page 69-70; 105pp; English.

XX A chimeric human/porcine CD86 (B7-2) cell adhesion molecule has amino  
CC acid residues 1-4 and 197-245 from human CD86, and amino acids 5-196 from  
CC porcine CD86. It is encoded by a DNA construct (AAT62939) obtd. by PCR  
CC amplification of porcine sequences and ligation to a sequence encoding  
CC the C-terminal region of human CD86 Igc domain. A signal sequence  
CC facilitates efficient secretion from transfected mammalian cells.  
CC Antibodies to porcine CD86 protein, P-selectin (see also AAM14945) and  
CC vascular cell adhesion molecule (see also AAM14931-42) are useful for  
CC diagnosing human rejection of porcine xenotransplants and for improving  
CC xenotransplantation of porcine cells, tissues and organs into human  
CC recipients. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 250 AA;

Query Match 23.0%; Score 76; DB 2; Length 250;  
Best Local Similarity 100.0%; Pred. No. 6.8e-65;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 FWQDDNIVLYELVYRGOKPHNNNSKVMGRSFOQATLTTLNHNVOIKDGSYCCFTHHK 109  
DB 56 FWQDDNIVLYELVYRGOKPHNNNSKVMGRSFOQATLTTLNHNVOIKDGSYCCFTHHK 115

QY 110 GPHGLVPIHOMSSDLS 125  
DB 116 GPHGLVPIHOMSSDLS 131

RESULT 4  
ID AAY32278 standard; protein; 329 AA.  
AC AAY32278;

DT 12-SEP-2003 (revised)  
DT 15-FEB-2000 (first entry)  
XX Cat CD86 (B7-2) ligand.

XX CD86; B7-2; ligand; cat; vaccine; feline immunodeficiency virus; FIV;  
XX feline leukaemia virus; feline infectious peritonitis virus;  
XX feline panleukopaemia virus; feline calicivirus; feline reovirus-3;  
XX feline rotavirus; feline coronavirus; feline syncytial virus;  
XX feline sarcoma virus; feline herpesvirus; feline Borna disease;  
XX rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;  
XX parasite; autoimmune disease; transplant rejection; therapy.

XX Felis catus.  
XX WO9957271-A2.  
XX 11-NOV-1999.  
XX 30-APR-1999; 99WO-US009502.  
XX 01-MAY-1998; 98US-00071699.  
XX (TEXA ) TEXAS A & M SYSTEM.

PI Collison EW, Haeh SM, Choi I;  
DR WPI; 2000-052972/04.  
DR N-PSDB; AA234785.  
XX Novel feline proteins used to produce feline vaccines which prevent  
PT infectious disease or to promote growth in homologous or heterologous  
PT species.  
XX Example 1A; Fig 3A; 186pp; English.

XX The present sequence represents feline CD86 (B7-2) ligand, as predicted  
CC from isolated cDNA of peripheral blood mononuclear cells. The  
CC coexpression of CD86 with the costimulatory molecules CD28 (see AAY32279)  
CC and a tumour antigen or an antigen from a pathogenic organism has the  
CC ability to activate or enhance activation of T-lymphocytes. Coexpression  
CC of CD86 with CTLA-4 (see AAY32280) has the ability to regulate activation  
CC of T-lymphocytes. The invention provides isolated nucleic acids encoding  
CC feline CD86 ligand, feline CD80 (B7-1) ligand, feline CD28 receptor or  
CC feline CTLA-4 (CD152) receptor, as well as vectors comprising the nucleic  
CC acids, and polypeptides encoded by the nucleic acids. It also provides  
CC vaccines comprising the CD86, CD86, CD28 or CTLA-4 polypeptides and  
CC further comprising immunogens derived from pathogens, especially feline  
CC immunodeficiency virus (FIV), feline leukaemia virus, feline infectious  
CC peritonitis virus, feline panleukopaemia virus, feline calicivirus,  
CC feline reovirus-3, feline rotavirus, feline coronavirus, feline syncytial  
CC virus, feline sarcoma virus, feline herpesvirus, feline Borna disease  
CC virus, rabies virus, chlamydia, Toxoplasmosis gondii, Dirofilaria  
CC immitis, or a flag, bacterial pathogen, or parasite (all claimed).  
CC vaccines capable of enhancing an immune response, and vaccines capable of  
CC suppressing an immune response (suitable for treating an autoimmune  
CC disease or tissue or organ transplant rejection) are claimed. (Updated on  
CC 12-SEP-2003 to standardise OS field)

XX Sequence 329 AA;

Query Match 4.2%; Score 14; DB 3; Length 329;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVOIKDKG 100  
 |||||  
 94 WTLRLHNVOIKDKG 107

RESULT 5  
 ID AAY32285  
 AAAY32285 standard; protein; 329 AA.  
 XX  
 AC AAY32285;  
 DT 12-SEP-2003 (revised)  
 DT 28-FEB-2000 (first entry)  
 XX  
 DE Feline CD86 (B7-2).  
 XX  
 KM CD86; B7-2; feline; cat; recombinant virus; vaccine; immunomodulator;  
 KM tumour; cancer; therapy.  
 XX  
 OS Feline catus.  
 XX  
 PN MO957295-A1.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 30-APR-1999; 99WO-US009504.  
 XX  
 PR 01-MAY-1998; 98US-00071711.  
 XX  
 PA (SCHE) SCHERING-PLOUGH LTD.  
 PA (SCHE) SCHERING-PLOUGH VETERINARY CORP.  
 XX  
 PI Winslow BJ, Cochran MD;  
 PI WPI; 2000-062155/05.  
 DR N-PSDB; AA234838.  
 XX  
 PT Novel recombinant virus useful as immunomodulators, particularly in  
 PT vaccines.  
 XX  
 PS Disclosure; Fig 3A; 230pp; English.  
 XX  
 CC This sequence represents feline CD86 (B7-2), as deduced from peripheral  
 CC blood mononuclear cell cDNA (see AA234838). Manipulating the expression  
 CC of CD28 or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)  
 CC regulates T cell proliferation and cytokine release. The invention  
 CC relates to a recombinant virus that contains at least one foreign nucleic  
 CC acid, inserted into a nonessential genomic region, that encodes feline  
 CC CD28, CD80, CD86 or CTLA-4 protein, or their immunogenic fragments, and  
 CC is expressed when the recombinant virus is introduced into a suitable  
 CC host. The invention also provides: a recombinant virus further comprising  
 CC a foreign nucleic acid encoding an immunogen derived from a feline  
 CC pathogen; recombinant viruses capable of enhancing an immune response to  
 CC protect against disease; recombinant viruses expressing antisense  
 CC sequences, capable of suppressing an immune response in a feline, e.g.  
 CC for treatment of autoimmune disease or transplant rejection; and  
 CC recombinant viruses expressing DNA encoding CD80 and/or CD86 used to  
 CC reduce or eliminate a tumour in cats. (Updated on 12-SEP-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 329 AA;

Query Match 4.2%; Score 14; DB 3; Length 329;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVOIKDKG 100  
 |||||  
 94 WTLRLHNVOIKDKG 107

RESULT 6  
 ID AA017734  
 AA017734 standard; protein; 329 AA.  
 XX  
 AC AA017734;  
 DT 08-AUG-2002 (first entry)  
 XX  
 DE Feline CD86.  
 XX

KM Cat; CD28; CD80; CTLA-4; CD86; immunogen; vaccine; viral infection;  
 KM feline immunodeficiency disease; feline infectious peritonitis;  
 KM feline leukaemia virus; cancer; degenerative disease; autoimmune disease;  
 KM viricide; immunomodulator; cytostatic; immunodeficiency.  
 XX  
 OS Feline catus.  
 XX  
 PN US2002051792-A1.  
 XX  
 PD 02-MAY-2002.  
 XX  
 PF 30-APR-1999; 99US-00303040.  
 XX  
 PR 01-MAY-1998; 98US-0083870P.  
 XX  
 PA (WINS/) WINSLOW B J.  
 PA (COCH/) COCHRAN M D.  
 XX  
 PI Winslow BJ, Cochran MD;  
 PI WPI; 2002-415200/44.  
 DR N-PSDB; AA146840.  
 XX  
 PT New recombinant virus, useful for immunizing felines to prevent or treat  
 PT feline immunodeficiency virus, comprises foreign nucleic acid encoding  
 PT feline cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or  
 PT CTLA-4.  
 XX  
 PS Disclosure; Fig 3; 77pp; English.  
 XX  
 CC The present invention relates to a recombinant virus comprising at least  
 CC one foreign nucleic acid encoding a protein selected from feline  
 CC cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or CTLA-4,  
 CC which is capable of expression when the virus is introduced into an  
 CC appropriate host. The virus can be administered to the feline in order to  
 CC elicit or enhance an immune response to prevent or treat feline  
 CC immunodeficiency disease, feline leukaemia, feline infectious peritonitis,  
 CC cancers, degenerative and autoimmune diseases and immunodeficiency. The  
 CC present sequence is a cytotoxic T lymphocyte accessory molecule described  
 CC in the exemplification of the invention  
 XX  
 SQ Sequence 329 AA;

Query Match 4.2%; Score 14; DB 5; Length 329;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVOIKDKG 100  
 |||||  
 94 WTLRLHNVOIKDKG 107

RESULT 7  
 ID AAU78121  
 AAU78121 standard; protein; 329 AA.  
 XX  
 AC AAU78121;  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE Feline CD86 protein.



XX Cat; vaccine; feline immunodeficiency virus; FIV; immunosuppressant;  
 KM feline infectious peritonitis; CD80 ligand; CD86 ligand; CD28; receptor;  
 KM CTLA-4; vaccine; rabies; autoimmune disease; organ transplant; feline leukemia;  
 KM toxoplasmosis gondii; flea; parasite; panleukopenia; feline leukaemia;  
 KM FelV; calicivirus; rotavirus; reovirus type 3; coronavirus; herpes;  
 XX borna disease.  
 OS Felis sp.  
 XX US2002028208-A1.  
 XX 07-MAR-2002.  
 XX 30-APR-1999; 99US-00303510.  
 XX 01-MAY-1998; 98US-0083669P.  
 XX (COLL/) COLLISON E W.  
 XX (HASH/) HASH S M.  
 XX (CHOI/) CHOI I.  
 XX COLLISON EW, Hash SM, Choi I;  
 XX WPI, 2002-315045/35.  
 XX N-PDB; ABK48230.  
 XX Polynucleotide encoding polypeptide of CD80 ligand, CD86 ligand, CD28  
 PT receptor or CTLA-4 receptor as vaccine for inducing immune response in  
 PT feline suffering from autoimmune disease or tissue or organ transplant.  
 PS Disclosure; Fig 3a; 73pp; English.  
 XX This invention relates to the DNA and protein sequences encoding a  
 CC soluble CD80 ligand, soluble CD86 ligand, soluble and membrane-bound CD28  
 CC receptor and soluble or membrane bound CTLA-4 receptor. The invention  
 CC also relates to a vaccine comprising an effective amount of these  
 CC receptor proteins. A vaccine is useful for inducing immunity or enhancing  
 CC an immune response in a cat. The protein sequences of the invention are  
 CC useful for suppressing an immune response in a feline suffering from an  
 CC autoimmune disease or the recipient of a tissue or organ transplant. A  
 CC vector containing the DNA sequences of the invention is useful for  
 CC redirecting an immune response in a feline to an immunogen such as rabies  
 CC virus, chlamydia, toxoplasmosis gondii, flea, feline immunodeficiency  
 CC virus, feline leukemia (FeLV), feline infectious peritonitis virus  
 CC (FIP), panleukopenia virus, calicivirus, reovirus type 3, rotavirus,  
 CC coronavirus, syncytial virus, herpes virus, sarcoma virus, borna disease  
 CC virus or a parasite. The protein sequences may be further utilised to  
 CC promote growth in homologous or heterologous feline species. Enhancement  
 CC of immunity through the interaction of soluble CD80 or soluble CD86 with  
 CC CD28 or CTLA-4 or inhibition of an immune response through the  
 CC interaction of feline CD80 or CD86 with CTLA-4 takes advantage of the  
 CC natural process of regulation rather than adding foreign substances that  
 CC could have multiple, even detrimental effects on overall or long term  
 CC health. The present sequence represents feline CD86 protein of the  
 CC invention.  
 XX SQ Sequence 329 AA;

Query Match 4.2%; Score 14; DB 5; Length 329;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKDKG 100  
 |||||  
 Db 94 WTLRLHNVQIKDKG 107

RESULT 8  
 AAY41079  
 ID AAY41079 standard; protein; 332 AA.  
 XX  
 AC AAY41079;

XX 20-DEC-1999 (first entry)  
 DT XX  
 DE Feline B7-2 protein.  
 XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;  
 KM allergic reaction; infectious disease; tumor development; feline;  
 KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.  
 XX  
 OS Felis catus.  
 XX WO9947558-A2.  
 XX 23-SEP-1999.  
 XX 19-MAR-1999; 99WO-US006187.  
 XX 19-MAR-1998; 98US-0078765P.  
 XX 17-APR-1998; 98US-00062597.  
 XX (HESK-) HESKA CORP.  
 XX Sim G, Yang S, Sellins KS;  
 XX WPI, 1999-571822/48  
 XX N-PDB; AA227929; AA227931.  
 XX New isolated B7 and CTLA4 nucleic acids, used to develop products for  
 PT treating, e.g. autoimmune and atopic diseases.  
 PT  
 PS Claim 4; Page 116-119; 148pp; English.  
 XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)  
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be  
 CC expressed by standard recombinant methodology. The nucleic acid molecules  
 CC and the encoded proteins can be used for preventing or treating diseases,  
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor  
 CC development, graft rejection, inflammation, arthritic and atopic diseases  
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,  
 CC cats, cattle, sheep or pets. The products can also be used for detection,  
 CC diagnosis and drug screening  
 XX SQ Sequence 332 AA;

Query Match 4.2%; Score 14; DB 2; Length 332;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKDKG 100  
 |||||  
 Db 94 WTLRLHNVQIKDKG 107

RESULT 9  
 AAY95333  
 ID AAY95333 standard; peptide; 30 AA.  
 XX  
 AC AAY95333;  
 XX  
 DT 12-SEP-2003 (revised)  
 DT 25-SEP-2000 (first entry)  
 DE  
 XX OVA323-339-pig costimulatory molecule B7-2 epitope hybrid peptide 10.  
 KM Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;  
 KM xerograft transplantation; organ transplant; vaccine; B-cell epitope;  
 KM T-cell epitope; ovalbumin; chicken.  
 XX  
 OS Gallus sp.  
 OS Sus scrofa.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers

```

FT Peptide 1..17
FT /note= "OVA323-339"
FT 18..30
FT Peptide /note= "B7-2 amino acids 76-88"
XX
XX WO200037102-A2.
XX
XX PD 29-JUN-2000.
XX
XX PF 17-DEC-1999; 99WO-GB004200.
XX
XX PR 19-DEC-1998; 98GB-00027921.
XX 23-OCT-1999; 99GB-00025015.
XX
XX PA (MLML-) ML LAB PLC.
XX
XX PI Lechler RI, Rogers NJ, Dorling A;
XX WPI; 2000-442537/38.
XX
XX PT Novel methods for improving tolerance to a xenograft comprising
XX immunizing a mammal with a T-cell epitope and a B-cell epitope.
XX
XX PS Disclosure; Page 23; 81pp; English.
XX
XX CC The present sequence is that of chimeric peptide 10 comprising T-cell
XX epitope OVA323-339 from chicken egg albumin (ovalbumin) and a B-cell
XX epitope comprising amino acids 76-88 of pig co-stimulatory molecule CD86
XX (B7-2) (see AAY95321). The invention relates to a novel strategy for
XX inhibiting costimulation by porcine cells of human T cells, with
XX particular importance in the context of xenotransplantation of porcine
XX organs. Recipients are immunised with hybrid synthetic peptides, such as
XX the present peptide, comprising a T cell epitope conjugated to sequences
XX of the porcine costimulatory molecules CD80, CD86 or CD40. Peptides that
XX induce antibodies specific for regions of costimulatory molecules
XX involved in binding to their counter-receptors on human cells are capable
XX of blocking the delivery of costimulation. Once the antibody response has
XX been induced, the transplanted organ will recall this response due to the
XX expression of the costimulatory molecules, thereby sustaining the
XX response, and providing an endogenous mechanism of costimulatory
XX blockade. The method is useful for improving the tolerance of a host to
XX xenografts, particularly porcine pancreatic islet cells. (Updated on 12-
XX SEP-2003 to standardise OS field)
XX
XX SQ Sequence 30 AA;
XX
XX Query Match 3.9%; Score 13; DB 3; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 0.00011;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 76 YMGRTSPDQATWT 88
XX |||||
XX 18 YMGRTSPDQATWT 30
XX
XX Db
XX
XX RESULT 10
XX AAY95327
XX ID AAY95327 standard; peptide; 30 AA.
XX
XX AC AAY95327;
XX
XX XX
XX DT 12-SEP-2003 (revised)
XX DT 25-SEP-2000 (first entry)
XX
XX XX
XX DE OVA323-339-pig costimulatory molecule B7-2 epitope hybrid peptide 3.
XX
XX XX Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;
XX KM xenotransplantation; organ transplant; vaccine; B-cell epitope;
XX KM T-cell epitope; ovalbumin; chicken.
XX
XX OS Gallus sp.
XX OS Sus scrofa.
XX OS Chimeric.

```

```

XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..17
XX FT /note= "OVA323-339"
XX FT 18..30
XX FT Peptide /note= "B7-2 amino acids 109-121"
XX
XX XX WO200037102-A2.
XX
XX XX PD 29-JUN-2000.
XX
XX XX PF 17-DEC-1999; 99WO-GB004200.
XX
XX XX PR 19-DEC-1998; 98GB-00027921.
XX 23-OCT-1999; 99GB-00025015.
XX
XX XX PA (MLML-) ML LAB PLC.
XX
XX XX PI Lechler RI, Rogers NJ, Dorling A;
XX XX WPI; 2000-442537/38.
XX
XX XX PT Novel methods for improving tolerance to a xenograft comprising
XX immunizing a mammal with a T-cell epitope and a B-cell epitope.
XX
XX XX PS Disclosure; Page 23; 81pp; English.
XX
XX CC The present sequence is that of chimeric peptide 3 comprising T-cell
XX epitope OVA323-339 from chicken egg albumin (ovalbumin) and a B-cell
XX epitope comprising amino acids 109-121 of pig co-stimulatory molecule
XX CD86 (B7-2) (see AAY95321). The invention relates to a novel strategy for
XX inhibiting costimulation by porcine cells of human T cells, with
XX particular importance in the context of xenotransplantation of porcine
XX organs. Recipients are immunised with hybrid synthetic peptides, such as
XX the present peptide, comprising a T cell epitope conjugated to sequences
XX of the porcine costimulatory molecules CD80, CD86 or CD40. Peptides that
XX induce antibodies specific for regions of costimulatory molecules
XX involved in binding to their counter-receptors on human cells are capable
XX of blocking the delivery of costimulation. Once the antibody response has
XX been induced, the transplanted organ will recall this response due to the
XX expression of the costimulatory molecules, thereby sustaining the
XX response, and providing an endogenous mechanism of costimulatory
XX blockade. The method is useful for improving the tolerance of a host to
XX xenografts, particularly porcine pancreatic islet cells. (Updated on 12-
XX SEP-2003 to standardise OS field)
XX
XX SQ Sequence 30 AA;
XX
XX Query Match 3.9%; Score 13; DB 3; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 0.00011;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 109 KGPFGLVPIHOMS 121
XX |||||
XX 18 KGPFGLVPIHOMS 30
XX
XX Db
XX
XX RESULT 11
XX AAY41080
XX ID AAY41080 standard; protein; 169 AA.
XX
XX AC AAY41080;
XX
XX XX
XX DT 20-DEC-1999 (first entry)
XX DT
XX XX
XX DE Feline B7-2 protein (larger fragment).
XX
XX XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX KM allergic reaction; infectious disease; tumor development; feline;
XX KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX OS Felis catus.
XX

```

```

PN WO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US006187.
XX
XX 19-MAR-1998; 98US-0078765P.
XX 17-APR-1998; 98US-00062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI; 1999-571822/48.
XX N-PSDB; AA27933.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases.
XX
XX Claim 4; Page 125-126; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritic and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening
XX
XX Sequence 169 AA;
XX
XX Query Match 3.9%; Score 13; DB 2; Length 169;
XX Best Local Similarity 100.0%; Pred. No. 0.00056;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 264 TLRRKKKOPGPS 276
XX |||||
XX 110 TLRRKKKOPGPS 122
XX
XX RESULT 12
XX AA41078
XX ID AA41078 standard; protein; 280 AA.
XX
XX AA41078;
XX
XX 20-DEC-1999 (first entry)
XX
XX Canine B7-2S protein.
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; canine;
XX graft rejection; inflammation; arthritis; atopic dermatitis.
XX
XX Canis familiaris.
XX
XX WO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US006187.
XX
XX 19-MAR-1998; 98US-0078765P.
XX 17-APR-1998; 98US-00062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI; 1999-571822/48.
XX N-PSDB; AA27921, AA27923.

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XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases.
XX
XX Claim 4; Page 109-111; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritic and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening
XX
XX Sequence 280 AA;
XX
XX Query Match 3.9%; Score 13; DB 2; Length 280;
XX Best Local Similarity 100.0%; Pred. No. 0.0009;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 29 TGEIPICHFTNSGN 41
XX |||||
XX 35 TGEIPICHFTNSGN 47
XX
XX RESULT 13
XX AA41076
XX ID AA41076 standard; protein; 329 AA.
XX
XX AA41076;
XX
XX 20-DEC-1999 (first entry)
XX
XX Canine B7-2 protein.
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; canine;
XX graft rejection; inflammation; arthritis; atopic dermatitis.
XX
XX Canis familiaris.
XX
XX WO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US006187.
XX
XX 19-MAR-1998; 98US-0078765P.
XX 17-APR-1998; 98US-00062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI; 1999-571822/48.
XX N-PSDB; AA27913, AA27915.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases.
XX
XX Claim 4; Page 97-99; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritic and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening

```



CC response, and providing an endogenous mechanism of costimulatory  
 CC blockade. The method is useful for improving the tolerance of a host to  
 CC xenografts, particularly porcine pancreatic islet cells. (Updated on 12-  
 CC SEP-2003 to standardise OS field)  
 XX

SQ Sequence 29 AA;

Query Match 3.6%; Score 12; DB 3; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 0.001;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 ASLKSQAYFNET 29  
 |||||  
 Db 18 ASLKSQAYFNET 29

Search completed: December 15, 2004, 16:56:55  
 Job time : 158 secs

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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:50:43 ; Search time 39 Seconds

(without alignments)  
561.152 Million cell updates/sec

Title: US-09-868-605-14

Sequence: 1 MGLSNILFVWVLLSGAASL.....NIKTASDNTDPLKSL 330

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Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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4: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 325   | 98.5        | 325    | 4     | US-09-651-200-20  |
| 2          | 14    | 4.2         | 328    | 4     | US-09-651-200-18  |
| 3          | 14    | 4.2         | 328    | 4     | US-09-303-040-6   |
| 4          | 13    | 3.9         | 329    | 4     | US-09-651-200-19  |
| 5          | 12    | 3.6         | 95     | 3     | US-08-928-3838-10 |
| 6          | 12    | 3.6         | 303    | 4     | US-09-651-200-23  |
| 7          | 12    | 3.6         | 303    | 4     | US-09-441-411-15  |
| 8          | 12    | 3.6         | 303    | 4     | US-09-441-411-20  |
| 9          | 12    | 3.6         | 308    | 2     | US-08-456-104-4   |
| 10         | 12    | 3.6         | 309    | 3     | US-08-479-744A-23 |
| 11         | 12    | 3.6         | 309    | 3     | US-08-280-757B-23 |
| 12         | 12    | 3.6         | 309    | 3     | US-08-205-697A-21 |
| 13         | 12    | 3.6         | 309    | 3     | US-08-702-525-21  |
| 14         | 12    | 3.6         | 309    | 3     | US-09-651-200-22  |
| 15         | 12    | 3.6         | 309    | 4     | US-09-667-135-13  |
| 16         | 12    | 3.6         | 309    | 4     | US-09-425-762-23  |
| 17         | 12    | 3.6         | 309    | 4     | US-09-837-867A-21 |
| 18         | 12    | 3.6         | 309    | 4     | US-09-206-132-4   |
| 19         | 12    | 3.6         | 309    | 4     | US-09-441-411-13  |
| 20         | 12    | 3.6         | 309    | 4     | US-09-441-411-18  |
| 21         | 12    | 3.6         | 309    | 4     | US-09-441-411-24  |
| 22         | 12    | 3.6         | 309    | 5     | PCT-US95-02576-21 |
| 23         | 12    | 3.6         | 314    | 3     | US-08-205-697A-13 |
| 24         | 12    | 3.6         | 314    | 3     | US-08-702-525-13  |
| 25         | 12    | 3.6         | 314    | 4     | US-09-837-867A-13 |
| 26         | 12    | 3.6         | 314    | 4     | US-09-441-411-14  |
| 27         | 12    | 3.6         | 314    | 4     | US-09-441-411-19  |

|    |    |     |     |   |                     |                   |
|----|----|-----|-----|---|---------------------|-------------------|
| 28 | 12 | 3.6 | 314 | 5 | PCT-US95-02576-13   | Sequence 13, Appl |
| 29 | 12 | 3.6 | 339 | 4 | US-09-719-243-2     | Sequence 2, Appl  |
| 30 | 12 | 3.6 | 356 | 4 | US-09-441-411-11    | Sequence 11, Appl |
| 31 | 12 | 3.6 | 356 | 4 | US-09-441-411-12    | Sequence 12, Appl |
| 32 | 12 | 3.6 | 356 | 4 | US-09-441-411-16    | Sequence 16, Appl |
| 33 | 12 | 3.6 | 356 | 4 | US-09-441-411-17    | Sequence 17, Appl |
| 34 | 12 | 3.6 | 358 | 4 | US-09-719-243-3     | Sequence 3, Appl  |
| 35 | 10 | 3.0 | 16  | 3 | US-08-205-687A-42   | Sequence 42, Appl |
| 36 | 10 | 3.0 | 16  | 3 | US-08-702-525-42    | Sequence 42, Appl |
| 37 | 10 | 3.0 | 16  | 4 | US-09-837-867A-42   | Sequence 42, Appl |
| 38 | 10 | 3.0 | 16  | 5 | PCT-US95-02576-42   | Sequence 42, Appl |
| 39 | 10 | 3.0 | 102 | 4 | US-09-513-999C-4502 | Sequence 4502, Ap |
| 40 | 10 | 3.0 | 110 | 3 | US-08-479-744A-45   | Sequence 45, Appl |
| 41 | 10 | 3.0 | 110 | 3 | US-08-280-757B-45   | Sequence 45, Appl |
| 42 | 10 | 3.0 | 110 | 4 | US-09-425-762-45    | Sequence 45, Appl |
| 43 | 10 | 3.0 | 323 | 4 | US-09-651-200-21    | Sequence 21, Appl |
| 44 | 10 | 3.0 | 323 | 4 | US-09-441-411-22    | Sequence 22, Appl |
| 45 | 10 | 3.0 | 323 | 5 | PCT-US94-09642-2    | Sequence 2, Appl  |

## ALIGNMENTS

RESULT 1  
US-09-651-200-20  
Sequence 20, Application US/09651200  
Patent No. 6429303  
GENERAL INFORMATION:  
APPLICANT: Green et al  
TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
FILE REFERENCE: 15966-563 (Cura-62)  
CURRENT APPLICATION NUMBER: US/09/651,200  
PRIOR FILING DATE: 2000-08-30  
PRIOR APPLICATION NUMBER: 60/152383  
PRIOR FILING DATE: 1999-09-03  
PRIOR APPLICATION NUMBER: 60/172909  
PRIOR FILING DATE: 1999-12-21  
PRIOR APPLICATION NUMBER: 60/183578  
PRIOR FILING DATE: 2000-02-18  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 20  
LENGTH: 325  
TYPE: PRT  
ORGANISM: Sus sp.  
US-09-651-200-20

Query Match 98.5%; Score 325; DB 4; Length 325;  
Best Local Similarity 100.0%; Pred. No. 1.3e-117;  
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |                                                            |     |
|----|-----|------------------------------------------------------------|-----|
| QY | 1   | MGLSNILFVWVLLSGAASLKSQAYFNETGELPHFTNSQLSLDELIVFQDDNLVLY    | 60  |
| DB | 1   | MGLSNILFVWVLLSGAASLKSQAYFNETGELPHFTNSQLSLDELIVFQDDNLVLY    | 60  |
| QY | 61  | ELVROGKPHVNVSKYMGRTSFDQATWTLRLAHVQIQDKSGYQCFIHKKGHGLVPIHOM | 120 |
| DB | 61  | ELVROGKPHVNVSKYMGRTSFDQATWTLRLAHVQIQDKSGYQCFIHKKGHGLVPIHOM | 120 |
| QY | 121 | SSDSLILNFQPEINILTNHTENSVINLTSSIQGYPEPQRMVMLNTKSTTEHDADY    | 180 |
| DB | 121 | SSDSLILNFQPEINILTNHTENSVINLTSSIQGYPEPQRMVMLNTKSTTEHDADY    | 180 |
| QY | 181 | KKSQNIITELNVSRVSLPPEPTNVSIVCVLQLEPSKTLFSLPCNIDAKPPVQPFVP   | 240 |
| DB | 181 | KKSQNIITELNVSRVSLPPEPTNVSIVCVLQLEPSKTLFSLPCNIDAKPPVQPFVP   | 240 |
| QY | 241 | DHILMIALVTVVVCNVSFTVLRKRKKQPGPSNECGATTIKNRKASQTKRRAEVH     | 300 |
| DB | 241 | DHILMIALVTVVVCNVSFTVLRKRKKQPGPSNECGATTIKNRKASQTKRRAEVH     | 300 |

QY 301 ERSDACQDVNIKTASDNDSTDP 325  
| | | | |  
Db 301 ERSDACQDVNIKTASDNDSTDP 325

RESULT 2  
US-09-651-200-18  
; Sequence 18, Application US/09651200  
; Patent No. 6429303  
; GENERAL INFORMATION:  
; APPLICANT: Green et al  
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 15966-562 (CURA-62)  
; CURRENT APPLICATION NUMBER: US/09/651,200  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/152383  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 60/172909  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 60/183578  
; PRIOR FILING DATE: 2000-02-18  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 329  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-651-200-18

Query Match 4.2%; Score 14; DB 4; Length 329;  
Best Local Similarity 100.0%; Pred. No. 1.e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKDKG 100  
| | | | |  
Db 94 WTLRLHNVQIKDKG 107

RESULT 3  
US-09-303-040-6  
; Sequence 6, Application US/09303040  
; Patent No. 6555671  
; GENERAL INFORMATION:  
; APPLICANT: Winslow, Barbara J.  
; APPLICANT: Cochran, Mark D.  
; TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding  
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CTLA-4 or  
; TITLE OF INVENTION: Feline Interferon-gamma And Uses Thereof  
; FILE REFERENCE: 54957-B  
; CURRENT APPLICATION NUMBER: US/09/303,040  
; CURRENT FILING DATE: 1999-04-30  
; EARLIER APPLICATION NUMBER: 60/083,870  
; EARLIER FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 329  
; TYPE: PRT  
; ORGANISM: feline CD86  
US-09-303-040-6

Query Match 4.2%; Score 14; DB 4; Length 329;  
Best Local Similarity 100.0%; Pred. No. 1.e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKDKG 100  
| | | | |  
Db 94 WTLRLHNVQIKDKG 107

RESULT 4

US-09-651-200-19  
; Sequence 19, Application US/09651200  
; Patent No. 6429303  
; GENERAL INFORMATION:  
; APPLICANT: Green et al  
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 15966-562 (CURA-62)  
; CURRENT APPLICATION NUMBER: US/09/651,200  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/152383  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 60/172909  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 60/183578  
; PRIOR FILING DATE: 2000-02-18  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 329  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-09-651-200-19

Query Match 3.9%; Score 13; DB 4; Length 329;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TGEIPLCHFTNSON 41  
| | | | |  
Db 35 TGEIPLCHFTNSON 47

RESULT 5  
US-08-928-383B-10  
; Sequence 10, Application US/08928383B  
; Patent No. 6210921  
; GENERAL INFORMATION:  
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,  
; APPLICANT: and Marshall S. Horvitz  
; TITLE OF INVENTION: CAR, A No. 6210921e1 Coxsackievirus and Adenovirus  
; TITLE OF INVENTION: Receptor  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/928,383B  
; FILING DATE: 12-SEP-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/026,100  
; FILING DATE: 13-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: DFN-020  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 95 amino acids



TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-928-383B-10

Query Match 3.6%; Score 12; DB 3; Length 95;  
Best Local Similarity 100.0%; Pred. No. 0.00035;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVOIKD 98  
Db 61 WTLRLHNVOIKD 72

RESULT 6  
US-09-651-200-23  
Sequence 23, Application US/09651200  
Patent No. 6429303  
GENERAL INFORMATION:  
APPLICANT: Green et al  
TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
TITLE OF INVENTION: Polypeptides Encoded Thereby  
FILE REFERENCE: 15966-562 (CURA-62)  
CURRENT APPLICATION NUMBER: US/09/651,200  
CURRENT FILING DATE: 2000-08-30  
PRIOR APPLICATION NUMBER: 60/152383  
PRIOR FILING DATE: 1999-09-03  
PRIOR APPLICATION NUMBER: 60/172909  
PRIOR FILING DATE: 1999-12-21  
PRIOR APPLICATION NUMBER: 60/183578  
PRIOR FILING DATE: 2000-02-18  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 23  
LENGTH: 303  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-651-200-23

Query Match 3.6%; Score 12; DB 4; Length 303;  
Best Local Similarity 100.0%; Pred. No. 0.001;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVOIKD 98  
Db 87 WTLRLHNVOIKD 98

RESULT 7  
US-09-441-411-15  
Sequence 15, Application US/09441411  
Patent No. 6734172  
GENERAL INFORMATION:  
APPLICANT: Scholler, Nathalie B.  
APPLICANT: Disis, Mary L.  
APPLICANT: Hellstrom, Ingegerd  
APPLICANT: Hellstrom, Karl Erik  
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES  
FILE REFERENCE: 730033.409  
CURRENT APPLICATION NUMBER: US/09/441,411  
CURRENT FILING DATE: 1999-11-16  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 303  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-441-411-15  
Query Match 3.6%; Score 12; DB 4; Length 303;  
Best Local Similarity 100.0%; Pred. No. 0.001;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVOIKD 98  
Db 87 WTLRLHNVOIKD 98

RESULT 8  
US-09-441-411-20  
Sequence 20, Application US/09441411  
Patent No. 6734172  
GENERAL INFORMATION:  
APPLICANT: Scholler, Nathalie B.  
APPLICANT: Disis, Mary L.  
APPLICANT: Hellstrom, Ingegerd  
APPLICANT: Hellstrom, Karl Erik  
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES  
FILE REFERENCE: 730033.409  
CURRENT APPLICATION NUMBER: US/09/441,411  
CURRENT FILING DATE: 1999-11-16  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20  
LENGTH: 303  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-441-411-20

Query Match 3.6%; Score 12; DB 4; Length 303;  
Best Local Similarity 100.0%; Pred. No. 0.001;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVOIKD 98  
Db 87 WTLRLHNVOIKD 98

RESULT 9  
US-08-456-104-4  
Sequence 4, Application US/08456104  
Patent No. 5861310  
GENERAL INFORMATION:  
APPLICANT: Freeman, Gordon J.  
APPLICANT: Nadler, Lee M.  
APPLICANT: Gray, Gary S.  
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/456,104  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/101,624;  
FILING DATE: 26-JUL-1993;  
APPLICATION NUMBER: 08/109,393;  
APPLICATION NUMBER: 19-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragoras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-008  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-456-104-4

Query Match 3.6%; Score 12; DB 2; Length 309;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 WTLRLHNVQIKD 98  
Db 93 WTLRLHNVQIKD 104

## RESULT 10

US-08-479-744A-23  
Sequence 23, Application US/08479744A

Patent No. 6084067  
GENERAL INFORMATION:

APPLICANT: Freeman, Gordon J.

APPLICANT: Nadler, Lee M.

TITLE OF INVENTION: No. 6084067e1 CTLA4/CD28 Ligands and

SOFTWARE: Patentin Release #1.0, Version #1.25

NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/479,744A

FILING DATE: June 7, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/280,757

FILING DATE: 26-JUL-1994

APPLICATION NUMBER: 08/109,393

FILING DATE: 28-AUG-1993

APPLICATION NUMBER: 08/101,624

FILING DATE: 26-JULY-1993

APPLICATION NUMBER: 08/147,773

FILING DATE: 3-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: RPI-004CP3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 309 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-479-744A-23

Qy 87 WTLRLHNVQIKD 98  
Db 93 WTLRLHNVQIKD 104

RESULT 11  
US-08-280-757B-23  
Sequence 23, Application US/08280757B

Patent No. 6130316  
GENERAL INFORMATION:

APPLICANT: Freeman, Gordon J.

APPLICANT: Nadler, Lee M.

TITLE OF INVENTION: No. 6130316e1 CTLA4/CD28 Ligands and

SOFTWARE: Patentin Release #1.0, Version #1.25

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/280,757B

FILING DATE: 26-JUL-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/101,624

FILING DATE: 26-JULY-1993

APPLICATION NUMBER: 08/109,393

FILING DATE: 19-AUG-1993

APPLICATION NUMBER: 08/147,773

FILING DATE: 3-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: RPI-004CP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 309 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-280-757B-23

Query Match 3.6%; Score 12; DB 3; Length 309;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 WTLRLHNVQIKD 98  
Db 93 WTLRLHNVQIKD 104

RESULT 12  
US-08-205-697A-21  
Sequence 21, Application US/08205697A

Patent No. 6218510  
GENERAL INFORMATION:

APPLICANT: Sharpe, Arlene H.

APPLICANT: Borriello, Francescopaulo

APPLICANT: Freeman, Gordon J.

```

; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
; TITLE OF INVENTION: and Uses therefor
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205,697A
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BMT-120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-205-697A-21

Query Match          3.6%; Score 12; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      87 WTLRLHNVQIKD 98
      |||||
Db      93 WTLRLHNVQIKD 104

RESULT 13
US-08-702-525-21
; Sequence 21, Application US/08702525
; Patent No. 6294660
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Sharpe
; APPLICANT: Freeman, Gordon
; APPLICANT: Nadler, Lee
; TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
; TITLE OF INVENTION: Molecules and Uses therefor
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,525
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
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; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BMT-120CPUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-525-21

Query Match          3.6%; Score 12; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      87 WTLRLHNVQIKD 98
      |||||
Db      93 WTLRLHNVQIKD 104

RESULT 14
US-09-651-200-22
; Sequence 22, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT FILING DATE: 2000-08-30
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152363
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-651-200-22

Query Match          3.6%; Score 12; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      87 WTLRLHNVQIKD 98
      |||||
Db      93 WTLRLHNVQIKD 104

RESULT 15
US-09-667-135-33
; Sequence 33, Application US/09667135
; Patent No. 6521749
; GENERAL INFORMATION:
; APPLICANT: Vincent Ling
; APPLICANT: Kyriaki Damsel-Joannopoulos
; TITLE OF INVENTION: NOVEL GL50 MOLECULES AND USES THEREFOR
; FILE REFERENCE: GNN-007
; CURRENT APPLICATION NUMBER: US/09/667,135
; CURRENT FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
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;  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; OTHER INFORMATION:  
US-09-667-135-33

Query Match 3.6%; Score 12; DB 4; Length 309;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 87 WTLRLHNVQIKD 98  
| | | | | | | | | |  
Db 93 WTLRLHNVQIKD 104

Search completed: December 15, 2004, 17:01:49  
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: December 15, 2004, 17:00:25 ; Search time 144 Seconds

(without alignments)  
818,534 Million cell updates/sec

Title: US-09-868-605-14

Perfect score: 330

Sequence: 1 MGLSNILFWVLLSGASL.....NLTATSDNNTDPLKSL 330

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Word size : 0

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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15: /cgml2\_6/prodata/2/pubppa/US10C\_PUBCOMB.pep.\*  
16: /cgml2\_6/prodata/2/pubppa/US10C\_PUBCOMB.pep.\*  
17: /cgml2\_6/prodata/2/pubppa/US10\_NEW\_PUB.pep.\*  
18: /cgml2\_6/prodata/2/pubppa/US11\_NEW\_PUB.pep.\*  
19: /cgml2\_6/prodata/2/pubppa/US60\_NEW\_PUB.pep.\*  
20: /cgml2\_6/prodata/2/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 14    | 4.2         | 329    | 9  | US-09-303-510-6    |
| 2          | 14    | 4.2         | 329    | 9  | US-09-303-040-6    |
| 3          | 14    | 4.2         | 332    | 16 | US-10-790-396-26   |
| 4          | 13    | 3.9         | 169    | 16 | US-10-790-396-31   |
| 5          | 13    | 3.9         | 280    | 16 | US-10-790-396-17   |
| 6          | 13    | 3.9         | 329    | 16 | US-10-790-396-7    |
| 7          | 12    | 3.6         | 323    | 13 | US-10-087-192-1077 |
| 8          | 12    | 3.6         | 303    | 10 | US-09-441-411-15   |
| 9          | 12    | 3.6         | 303    | 10 | US-09-441-411-20   |
| 10         | 12    | 3.6         | 303    | 17 | US-10-762-128-15   |
| 11         | 12    | 3.6         | 303    | 17 | US-10-762-128-20   |
| 12         | 12    | 3.6         | 309    | 9  | US-09-425-762-23   |
| 13         | 12    | 3.6         | 309    | 9  | US-09-837-867A-21  |

|    |    |     |     |    |                   |                   |
|----|----|-----|-----|----|-------------------|-------------------|
| 14 | 12 | 3.6 | 309 | 10 | US-09-441-411-13  | Sequence 13, Appl |
| 15 | 12 | 3.6 | 309 | 10 | US-09-441-411-18  | Sequence 18, Appl |
| 16 | 12 | 3.6 | 309 | 10 | US-09-441-411-14  | Sequence 24, Appl |
| 17 | 12 | 3.6 | 309 | 10 | US-09-441-411-19  | Sequence 21, Appl |
| 18 | 12 | 3.6 | 309 | 15 | US-10-318-853-33  | Sequence 23, Appl |
| 19 | 12 | 3.6 | 309 | 17 | US-10-643-768-21  | Sequence 21, Appl |
| 20 | 12 | 3.6 | 309 | 17 | US-10-762-128-13  | Sequence 18, Appl |
| 21 | 12 | 3.6 | 309 | 17 | US-10-762-128-18  | Sequence 24, Appl |
| 22 | 12 | 3.6 | 309 | 17 | US-10-762-128-24  | Sequence 24, Appl |
| 23 | 12 | 3.6 | 309 | 17 | US-10-429-0798-23 | Sequence 23, Appl |
| 24 | 12 | 3.6 | 314 | 9  | US-09-837-867A-13 | Sequence 13, Appl |
| 25 | 12 | 3.6 | 314 | 10 | US-09-441-411-13  | Sequence 14, Appl |
| 26 | 12 | 3.6 | 314 | 10 | US-09-441-411-14  | Sequence 19, Appl |
| 27 | 12 | 3.6 | 314 | 10 | US-09-441-411-19  | Sequence 14, Appl |
| 28 | 12 | 3.6 | 314 | 10 | US-09-962-969-13  | Sequence 13, Appl |
| 29 | 12 | 3.6 | 314 | 17 | US-10-643-768-13  | Sequence 13, Appl |
| 30 | 12 | 3.6 | 314 | 17 | US-10-762-128-14  | Sequence 14, Appl |
| 31 | 12 | 3.6 | 314 | 17 | US-10-762-128-19  | Sequence 14, Appl |
| 32 | 12 | 3.6 | 339 | 15 | US-10-727-000-2   | Sequence 2, Appl  |
| 33 | 12 | 3.6 | 356 | 10 | US-09-441-411-11  | Sequence 2, Appl  |
| 34 | 12 | 3.6 | 356 | 10 | US-09-441-411-11  | Sequence 11, Appl |
| 35 | 12 | 3.6 | 356 | 10 | US-09-441-411-12  | Sequence 12, Appl |
| 36 | 12 | 3.6 | 356 | 10 | US-09-441-411-16  | Sequence 16, Appl |
| 37 | 12 | 3.6 | 356 | 17 | US-10-762-128-11  | Sequence 17, Appl |
| 38 | 12 | 3.6 | 356 | 17 | US-10-762-128-16  | Sequence 12, Appl |
| 39 | 12 | 3.6 | 356 | 17 | US-10-762-128-17  | Sequence 16, Appl |
| 40 | 12 | 3.6 | 358 | 15 | US-10-727-000-3   | Sequence 17, Appl |
| 41 | 10 | 3.0 | 16  | 9  | US-09-837-867A-42 | Sequence 3, Appl  |
| 42 | 10 | 3.0 | 16  | 9  | US-09-962-969-42  | Sequence 42, Appl |
| 43 | 10 | 3.0 | 16  | 17 | US-10-643-768-42  | Sequence 42, Appl |
| 44 | 10 | 3.0 | 104 | 16 | US-10-696-259-18  | Sequence 18, Appl |
| 45 | 10 | 3.0 | 110 | 9  | US-09-425-762-45  | Sequence 45, Appl |

#### ALIGNMENTS

RESULT 1  
US-09-303-510-6  
; Sequence 6, Application US/09303510A  
; Patent No. US2002028208A1  
; GENERAL INFORMATION:  
; APPLICANT: Collisson, Ellen W.  
; APPLICANT: Hash, Stephen M.  
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline  
; FILE REFERENCE: 54954  
; CURRENT APPLICATION NUMBER: US/09/303,510A  
; CURRENT FILING DATE: 1999-04-30  
; EARLIER APPLICATION NUMBER: 60/083,869  
; EARLIER FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 329  
; TYPE: PRT  
; ORGANISM: Feline  
US-09-303-510-6  
  
Query Match 4.2%; Score 14; DB 9; Length 329;  
Best Local Similarity 100.0%; Pred. No. 8.1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 87 WTLLRHVQIDKXG 100  
DB 94 WTLLRHVQIDKXG 107  
  
RESULT 2  
US-09-303-040-6  
; Sequence 6, Application US/09303040  
; Patent No. US20020051792A1

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; GENERAL INFORMATION:
; APPLICANT: Winslow, Barbara J.
; TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CTLA-4 or
; FILE REFERENCE: 54957-B
; CURRENT APPLICATION NUMBER: US/09/303,040
; PRIOR FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,870
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 329
; TYPE: PRT
; ORGANISM: feline CD86
US-09-303-040-6

Query Match          4.2% Score 14; DB 9; Length 329;
Best Local Similarity 100.0%; Pred.No. 8.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      87 WTLRLHNVQIKDKG 100
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Db      94 WTLRLHNVQIKDKG 107

RESULT 3
US-10-790-396-26
; Sequence 26, Application US/10790396
; Publication No. US20040157296A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
; FILE REFERENCE: IM-1-CI-PCT
; CURRENT APPLICATION NUMBER: US/10/790,396
; PRIOR FILING DATE: 2004-03-01
; PRIOR APPLICATION NUMBER: US/09/646,561
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/078,765
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 09/062,597
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Felis catus
US-10-790-396-26

Query Match          4.2% Score 14; DB 16; Length 332;
Best Local Similarity 100.0%; Pred.No. 8.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      87 WTLRLHNVQIKDKG 100
      |||||
Db      94 WTLRLHNVQIKDKG 107

RESULT 4
US-10-790-396-31
; Sequence 31, Application US/10790396
; Publication No. US20040157296A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Sellins, Karen S.
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
; PROTEINS, NUCLEIC
```

```

; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-1-CI-PCT
; CURRENT APPLICATION NUMBER: US/10/790,396
; PRIOR FILING DATE: 2004-03-01
; PRIOR APPLICATION NUMBER: US/09/646,561
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/078,765
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 09/062,597
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Felis catus
US-10-790-396-31

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Best Local Similarity 100.0%; Pred.No. 0.00042;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      264 TLRKRXKQPGPS 276
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Db      110 TLRKRXKQPGPS 122

RESULT 5
US-10-790-396-17
; Sequence 17, Application US/10790396
; Publication No. US20040157296A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
; FILE REFERENCE: IM-1-CI-PCT
; CURRENT APPLICATION NUMBER: US/10/790,396
; PRIOR FILING DATE: 2004-03-01
; PRIOR APPLICATION NUMBER: US/09/646,561
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/078,765
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 09/062,597
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-790-396-17

Query Match          3.9% Score 13; DB 16; Length 280;
Best Local Similarity 100.0%; Pred.No. 0.00066;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      29 TGLPCHFTNSON 41
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Db      35 TGLPCHFTNSON 47

RESULT 6
US-10-790-396-7
; Sequence 7, Application US/10790396
; Publication No. US20040157296A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Sellins, Karen S.
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
; PROTEINS, NUCLEIC
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Thu Dec 16 12:21:13 2004

us-09-868-605-14.01igo.rapb

Page 3

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FILE REFERENCE: IM-1-C1-PCT
CURRENT APPLICATION NUMBER: US/10/790,396
CURRENT FILING DATE: 2004-03-01
PRIOR APPLICATION NUMBER: US/09/646,561
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 60/078,765
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 09/062,597
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 329
TYPE: PRT
ORGANISM: Canis familiaris
US-10-790-396-7
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Query Match      3.9%; Score 13; DB 16; Length 329;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      29  TGEIPECHFTNSQN 41
DB      35  TGEIPECHFTNSQN 47
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RESULT 7
US-10-087-192-1077
Sequence 1077, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 52945200122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1077
LENGTH: 230
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)-(230)
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-087-192-1077
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Query Match      3.6%; Score 12; DB 13; Length 230;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      87  WTLRLHNVQIKD 98
DB      90  WTLRLHNVQIKD 101
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```
RESULT 8
US-09-441-411-15
Sequence 15, Application US/09441411
Publication No. US20030008342A1
GENERAL INFORMATION:
APPLICANT: Scholler, Nathalie B.
APPLICANT: Disis, Mary L.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
```

```
FILE REFERENCE: 730033.409
CURRENT APPLICATION NUMBER: US/09/441,411
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 303
TYPE: PRT
ORGANISM: Mus musculus
US-09-441-411-15
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Query Match      3.6%; Score 12; DB 10; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      87  WTLRLHNVQIKD 98
DB      87  WTLRLHNVQIKD 98
```

```
RESULT 9
US-09-441-411-20
Sequence 20, Application US/09441411
Publication No. US20030008342A1
GENERAL INFORMATION:
APPLICANT: Scholler, Nathalie B.
APPLICANT: Disis, Mary L.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
FILE REFERENCE: 730033.409
CURRENT APPLICATION NUMBER: US/09/441,411
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 303
TYPE: PRT
ORGANISM: Mus musculus
US-09-441-411-20
```

```
Query Match      3.6%; Score 12; DB 10; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      87  WTLRLHNVQIKD 98
DB      87  WTLRLHNVQIKD 98
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RESULT 10
US-10-762-128-15
Sequence 15, Application US/10762128
Publication No. US20040219161A1
GENERAL INFORMATION:
APPLICANT: Scholler, Nathalie B.
APPLICANT: Disis, Mary L.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
FILE REFERENCE: 730033.409C1
CURRENT APPLICATION NUMBER: US/10/762,128
CURRENT FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: US 09/441,411
PRIOR FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 303
TYPE: PRT
ORGANISM: Mus musculus
US-10-762-128-15
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Query Match 3.6%; Score 12; DB 17; Length 303;  
Best Local Similarity 100.0%; Pred. No. 0.0067;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKD 98  
DB 87 WTLRLHNVQIKD 98

RESULT 11  
US-10-762-128-20  
; Sequence 20, Application US/10762128  
; Publication No. US20040219161A1  
; GENERAL INFORMATION:  
; APPLICANT: Scholler, Nathalie B.  
; APPLICANT: Disis, Mary L.  
; APPLICANT: Hellstrom, Ingegerd  
; APPLICANT: Hellstrom, Karl Erik  
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES  
; FILE REFERENCE: 730033.409C1  
; CURRENT APPLICATION NUMBER: US/10/762,128  
; CURRENT FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: US 09/441,411  
; PRIOR FILING DATE: 1999-11-16  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 303  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-762-128-20

Query Match 3.6%; Score 12; DB 17; Length 303;  
Best Local Similarity 100.0%; Pred. No. 0.0067;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKD 98  
DB 87 WTLRLHNVQIKD 98

RESULT 12  
US-09-425-762-23  
; Sequence 23, Application US/09425762  
; Publication No. US20020086414A1  
; GENERAL INFORMATION:  
; APPLICANT: Freeman, Gordon J.  
; APPLICANT: Nadler, Lee M.  
; APPLICANT: Gray, Gary S.  
; TITLE OF INVENTION: No. 6605279e1 CTLA4/CD28 ligands and  
; TITLE OF INVENTION: Uses Therefor  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/425,762  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/479,744  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-004CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-425-762-23

Query Match 3.6%; Score 12; DB 9; Length 309;  
Best Local Similarity 100.0%; Pred. No. 0.0068;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKD 98  
DB 93 WTLRLHNVQIKD 104

RESULT 13  
US-09-837-867A-21  
; Sequence 21, Application US/09837867A  
; Patent No. US20020098542A1  
; GENERAL INFORMATION:  
; APPLICANT: Sharpe, Arlene H.  
; APPLICANT: Bottiello, Francescopaulo  
; APPLICANT: Freeman, Gordon J.  
; APPLICANT: Nadler, Lee M.  
; TITLE OF INVENTION: No. US0020098542A1e1 Forms of T Cell Costimulatory  
; TITLE OF INVENTION: Molecules and Uses Therefor  
; FILE REFERENCE: BWI-120CPADV  
; CURRENT APPLICATION NUMBER: US/09/837,867A  
; CURRENT FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 08/205,697  
; PRIOR FILING DATE: 1994-03-02  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-837-867A-21

Query Match 3.6%; Score 12; DB 9; Length 309;  
Best Local Similarity 100.0%; Pred. No. 0.0068;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKD 98  
DB 93 WTLRLHNVQIKD 104

RESULT 14  
US-09-441-411-13  
; Sequence 13, Application US/09441411  
; Publication No. US20030008342A1  
; GENERAL INFORMATION:  
; APPLICANT: Scholler, Nathalie B.  
; APPLICANT: Disis, Mary L.  
; APPLICANT: Hellstrom, Ingegerd  
; APPLICANT: Hellstrom, Karl Erik  
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES  
; FILE REFERENCE: 730033.409  
; CURRENT APPLICATION NUMBER: US/09/441,411  
; CURRENT FILING DATE: 1999-11-16  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 309  
; TYPE: PRT



Thu Dec 16 12:21:13 2004

us-09-868-605-14.Oligo.rapb

Page 5

ORGANISM: Mus musculus  
US-09-441-411-13

Query Match  
Best Local Similarity 100.0%; Score 12; DB 10; Length 309;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 87 WTLRLHNVQIKD 98  
|||||  
Db 93 WTLRLHNVQIKD 104

RESULT 15  
US-09-441-411-18  
; Sequence 18; Application US/09441411  
; Publication No. US20030008342A1  
; GENERAL INFORMATION:  
; APPLICANT: Scholler, Nathalie B.  
; APPLICANT: Disis, Mary L.  
; APPLICANT: Helstrom, Ingegerd  
; APPLICANT: Helstrom, Karl Erik  
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES  
; FILE REFERENCE: 730033.409  
; CURRENT APPLICATION NUMBER: US/09/441,411  
; CURRENT FILING DATE: 1999-11-16  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-441-411-18

Query Match  
Best Local Similarity 100.0%; Score 12; DB 10; Length 309;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 87 WTLRLHNVQIKD 98  
|||||  
Db 93 WTLRLHNVQIKD 104

Search completed: December 15, 2004, 17:12:44  
Job time : 145 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:50:10 ; Search time 40 Seconds  
(without alignments)  
793.788 Million cell updates/sec

Title: US-09-868-605-14

Perfect score: 330

Sequence: 1 MGLSNILFVMVLLSGAASL.....NLIKASPDNSTTDFIKSKL 330

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Query length | ID | Description        |
|------------|-------|-------------|--------------|----|--------------------|
| 1          | 12    | 3.6         | 309          | 2  | gene B7-2 protein  |
| 2          | 10    | 3.0         | 110          | 2  | CD86 spliced varia |
| 3          | 10    | 3.0         | 275          | 2  | CD86 spliced varia |
| 4          | 10    | 3.0         | 329          | 1  | B7-2 antigen - hum |
| 5          | 10    | 3.0         | 330          | 2  | CD86 precursor - r |
| 6          | 8     | 2.4         | 298          | 2  | hypothetical prote |
| 7          | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 8          | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 9          | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 10         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 11         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 12         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 13         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 14         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 15         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 16         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 17         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 18         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 19         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 20         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 21         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 22         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 23         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 24         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 25         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 26         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 27         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 28         | 8     | 2.4         | 354          | 2  | hypothetical prote |
| 29         | 8     | 2.4         | 354          | 2  | hypothetical prote |

|    |   |     |     |   |        |                    |
|----|---|-----|-----|---|--------|--------------------|
| 30 | 7 | 2.1 | 343 | 2 | S44721 | outer membrane pro |
| 31 | 7 | 2.1 | 347 | 2 | S15171 | outer membrane pro |
| 32 | 7 | 2.1 | 347 | 2 | S15172 | outer membrane pro |
| 33 | 7 | 2.1 | 347 | 2 | T35013 | probable membrane  |
| 34 | 7 | 2.1 | 348 | 2 | S15175 | outer membrane pro |
| 35 | 7 | 2.1 | 348 | 2 | S15170 | outer membrane pro |
| 36 | 7 | 2.1 | 348 | 2 | S44720 | outer membrane pro |
| 37 | 7 | 2.1 | 349 | 2 | S15173 | outer membrane pro |
| 38 | 7 | 2.1 | 350 | 2 | S44718 | outer membrane pro |
| 39 | 7 | 2.1 | 350 | 2 | S15176 | outer membrane pro |
| 40 | 7 | 2.1 | 350 | 2 | S44717 | outer membrane pro |
| 41 | 7 | 2.1 | 351 | 2 | S20537 | outer membrane pro |
| 42 | 7 | 2.1 | 352 | 2 | S15177 | outer membrane pro |
| 43 | 7 | 2.1 | 354 | 2 | S44724 | outer membrane pro |
| 44 | 7 | 2.1 | 354 | 2 | S22757 | outer membrane pro |
| 45 | 7 | 2.1 | 354 | 2 | S44725 | outer membrane pro |

#### ALIGNMENTS

##### RESULT 1

Gene B7-2 protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I49522  
R:Freeman, G.J.; Borriello, F.; Hodges, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim, J.  
J. Exp. Med. 178, 2185-2192, 1993  
A>Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell pr  
A:Reference number: I49522; MUID:94065585; PMID:7504059  
A:Accession: I49522  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-309 <RES>  
A:Cross-references: UNIPROT:P42082; GB:L25606; NID:G432478; PIDN:AAA79770.1; PID:G43247  
A:Genetics:  
A:Gene: B7-2  
C:Superfamily: B7-2 antigen

Query Match 3.6%; Score 12; DB 2; Length 309;  
Best Local Similarity 100.0%; Pred. No. 0.00039;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;

QY 87 WTLRLHNVQIKD 98  
DB 93 WTLRLHNVQIKD 104

##### RESULT 2

UC7605  
CD86 spliced variant CD86 deltaEC isoform - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
C:Accession: UC7605  
R:Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bonnefoy, J.Y.; Delneste, Y.  
Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001  
A>Title: Identification of an alternatively spliced variant of human CD86 mRNA.  
A:Reference number: UC7604; MUID:21092744; PMID:11162656  
A:Accession: UC7605  
A:Molecule type: mRNA  
A:Residues: 1-110 <MAG>  
A:Cross-references: UNIPROT:P42081  
C:Comment: This CD86 variant expressed by nonstimulated human monocytes, as a membrane  
A:Gene: cd86deltaEC

Query Match 3.0%; Score 10; DB 2; Length 110;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSNILFVM 10

Db 1 MGLSNILFVM 10

## RESULT 3

CD86 spliced variant CD86 deltaTM isoform - human  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 18-Nov-2002  
 C/Accession: J07604  
 R/Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bonnefoy, J.Y.; Delneste, Y.  
 Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001  
 A/Title: Identification of an alternatively spliced variant of human CD86 mRNA.  
 A/Reference number: J07604; MUID:21092744; PMID:11162656  
 A/Accession: J07604  
 A/Molecule type: mRNA  
 A/Residues: 1-275 <MAG>  
 C/Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory  
 C/Genetics:  
 A/Gene: cd86deltaTM  
 C/Superfamily: B-lymphocyte restricted antigen B7  
 C/Keywords: immune response

Query Match 3.0%; Score 10; DB 2; Length 275;

Best Local Similarity 100.0%; Pred. No. 0.042;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSNILFVM 10

Db 1 MGLSNILFVM 10

## RESULT 4

B7-2 antigen - human  
 N/Alternate names: B70 glycoprotein, CD86 antigen, CTLA-4 counter-receptor  
 C/Species: Homo sapiens (man)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: A48754; S39055  
 R/Freeman, G.J.; Gridben, J.G.; Boussoicis, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombard, S.  
 Science 262, 909-911, 1993  
 A/Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell proliferation.  
 A/Reference number: A48754; MUID:94053735; PMID:7694363  
 A/Accession: A48754  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-329 <FRE>  
 A/Cross-references: UNIPROT:P42081; GB:L25259; NID:G416368; PIDN:AAA58389.1; PID:G416369  
 A/Note: It is uncertain whether Met-1 or Met-7 is the initiator  
 R/Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza, C.  
 Nature 366, 76-79, 1993  
 A/Title: B70 antigen is a second ligand for CTLA-4 and CD28.  
 A/Reference number: S39055; MUID:94050123; PMID:7694153  
 A/Accession: S39055  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 7-329 <AZU>  
 A/Cross-references: GB:U04343; NID:G439838; PIDN:ABA03814.1; PID:G439839  
 C/Genetics:  
 A/Gene: GDB:CD86; CD28LG2  
 A/Cross-references: GDB:433597; OMIM:601020  
 A/Map position: 3q13.3-3q21  
 C/Superfamily: B7-2 antigen  
 C/Keywords: glycoprotein

Query Match 3.0%; Score 10; DB 1; Length 329;

Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSNILFVM 10

Db 7 MGLSNILFVM 16

## RESULT 5

CD86 precursor - rabbit  
 C/Species: Oryctolagus cuniculus (domestic rabbit)  
 C/Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 09-Jul-2004  
 C/Accession: I46691  
 R/Isono, T.; Sato, A.  
 Immunogenetics 42, 217-220, 1995  
 A/Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule CD86.  
 A/Reference number: I46689; MUID:9536949; PMID:7642234  
 A/Accession: I46691  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-330 <ISO>  
 A/Cross-references: UNIPROT:P42071; GB:D49842; NID:G755098; PIDN:BA08642.1; PID:G75509  
 C/Superfamily: B7-2 antigen

Query Match 3.0%; Score 10; DB 2; Length 330;

Best Local Similarity 100.0%; Pred. No. 0.05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 LHNVOIKDKG 100

Db 97 LHNVOIKDKG 106

## RESULT 6

hypothetical protein s110224 - Synechocystis sp. (strain PCC 6803)  
 C/Species: Synechocystis sp.  
 A/Variety: PCC 6803  
 C/Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
 C/Accession: S74562  
 R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.  
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, N.  
 DNA Res. 3, 109-136, 1996  
 A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.  
 A/Reference number: S74322; MUID:97061201; PMID:8905231  
 A/Accession: S74562  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-298 <KAN>  
 A/Cross-references: UNIPROT:P72707; EMBL:D90900; GB:AB001339; NID:G1651768; PIDN:BA0167  
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 2.4%; Score 8; DB 2; Length 298;

Best Local Similarity 100.0%; Pred. No. 5.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LLSGASL 20

Db 12 LLSGASL 19

## RESULT 7

yeast protein precursor - yeast (Saccharomyces cerevisiae)  
 N/Alternate names: glycoprotein 38; protein N171; protein YNL16W  
 C/Species: Saccharomyces cerevisiae  
 C/Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004  
 C/Accession: S60967; A56542; S63112; S63814; S33203  
 R/Nasr, F.; Becam, A.M.; Herbert, C.J.  
 submitted to the EMBL Data Library October 1995  
 A/Description: The sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 c  
 tonic dystrophy kinase.  
 A/Reference number: S60967  
 A/Accession: S60967  
 A/Molecule type: DNA  
 A/Residues: 1-354 <NAS>  
 A/Cross-references: UNIPROT:P38616; EMBL:X92517; NID:G1050783; PID:G1050792  
 R/Desnuelle, M.; Holzer, H.; Klionsky, D.J.

Mol. Cell. Biol. 14, 2740-2754, 1994  
 A>Title: Identification and characterization of a novel yeast gene: the YGP1 gene product  
 A/Reference number: A55542; MUID:94187744; PMID:8139573  
 A/Accession: A55542  
 A>Status: Preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-46, 'D', '48-78', 'R', '80-354' <DE>  
 A/Cross-references: GB:X73030; NID:9297484; PIDN:CAA51513.1; PID:9297485  
 A/Note: authors translated the codon ACT for residue 225 as Trp  
 R/Narr: F.; Becam, A.M.; Herbert, C.  
 Submitted to the Protein Sequence Database, April 1996  
 A/Reference number: S62967  
 A/Accession: S63112  
 A/Molecule type: DNA  
 A/Residues: 1-354 <NMF>  
 A/Cross-references: EMBL:Z71436; NID:G1302125; PID:e239816; PID:G1302126; MIPS:YNL160W  
 A/Experimental source: strain S286C  
 R/Narr: F.; Becam, A.M.; Herbert, C.J.  
 Yeast 12, 169-175, 1996  
 A>Title: The sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 complete  
 dysotrophy kinases.  
 A/Reference number: S63805; MUID:96287653; PMID:8686380  
 A/Accession: S63814  
 A>Status: nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-354 <NMF>  
 A/Cross-references: EMBL:X92517; NID:G1050783; PIDN:CAA63279.1; PID:G1050792  
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995  
 C/Genetics:  
 A/Gene: SGD:YGP1  
 A/Cross-references: SGD:S0005104; MIPS:YNL160W  
 A/Map position: 14L  
 C/Keywords: glycoprotein  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-354/Product: YGP1 protein #status predicted <MAT>

Query Match 2.4%; Score 8; DB 2; Length 354;  
 Best Local Similarity 100.0%; Pred. No. 6.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 NITELYNV 193  
 |||||  
 Db 106 NITELYNV 113

RESULT 8  
 S48394  
 probable membrane protein YIL140W - yeast (Saccharomyces cerevisiae)  
 C/Species: Saccharomyces cerevisiae  
 C/Date: 02-Dec-1994 #sequence\_revision 02-Dec-1994 #text\_change 09-Jul-2004  
 C/Accession: S48394; S50276  
 R/Churruarri, C.  
 Submitted to the EMBL Data Library, September 1994  
 A/Reference number: S48310  
 A/Accession: S48394  
 A/Molecule type: DNA  
 A/Residues: 1-823 <CHU>  
 A/Cross-references: UNIPROT:P38928; GB:Z47047; EMBL:Z38059; NID:G603997; PID:G763206; MI  
 R/Torpey, L.E.; Gibbs, P.E.W.; Nelson, J.; Lawrence, C.W.  
 Yeast 10, 1503-1509, 1994  
 A>Title: Cloning and sequence of REV7, a gene whose function is required for DNA damage-  
 A/Reference number: S50275; MUID:95176709; PMID:7871890  
 A/Accession: S50276  
 A>Status: nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 80-823 <TOR>  
 A/Cross-references: EMBL:U07228; NID:G460247; PIDN:AA67919.1; PID:G460249  
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994  
 C/Genetics:  
 A/Gene: SGD:SR04  
 A/Cross-references: SGD:S0001402; MIPS:YIL140W  
 A/Map position: 9L  
 C/Superfamily: Saccharomyces cerevisiae probable membrane protein YIL140W

C/Keywords: transmembrane protein  
 F:6-22/Domain: transmembrane #status predicted <TM>  
 F:511-527/Domain: transmembrane #status predicted <TM2>

Query Match 2.4%; Score 8; DB 2; Length 823;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 AKPPVQPP 238  
 |||||  
 Db 633 AKPPVQPP 640

RESULT 9  
 138418  
 HLA-A2 - human (fragment)  
 N/Alternate names: HLA-A23  
 C/Species: Homo sapiens (man)  
 C/Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
 C/Accession: 138418; 138419  
 R/Balas, A.; Garcia-Sanchez, F.; Gomez-Reino, F.; Vicario, J.L.  
 Hum. Immunol. 41, 69-73, 1994  
 A>Title: HLA class I allele (HLA-A2) expression defect associated with a mutation in its  
 A/Reference number: 138417; MUID:95137784; PMID:7836067  
 A/Accession: 138418  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-20 <RES>  
 A/Cross-references: UNIPROT:P01892; UNIPROT:O19620; EMBL:U02935; NID:G414545; PIDN:AAA7  
 A/Accession: 138419  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-20 <RES>  
 A/Cross-references: EMBL:U02936; NID:G414547; PIDN:AAA76609.1; PID:G414548  
 C/Genetics:  
 A/Gene: HLA-2; HLA-23  
 A/Map position: 6p21.3  
 C/Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 2.1%; Score 7; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VLLSGA 17  
 |||||  
 Db 10 VLLSGA 16

RESULT 10  
 A48972  
 mannose-specific lectin - ramson (fragment)  
 C/Species: Allium ursinum (ramson)  
 C/Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 28-Apr-1995  
 C/Accession: A48972  
 R/Kaku, H.; Goldstein, I.J.; Van Damme, E.J.; Peumans, W.J.  
 Carbohydr. Res. 229, 347-353, 1992  
 A>Title: New mannose-specific lectins from garlic (Allium sativum) and ramsons (Allium  
 A/Reference number: A48972; MUID:93008079; PMID:1394291  
 A/Accession: A48972  
 A>Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-34 <RAK>  
 A/Experimental source: bulb  
 A/Note: sequence extracted from NCBI backbone (NCBI:P:119584)

Query Match 2.1%; Score 7; DB 2; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 DNLVLYE 61  
 |||||  
 Db 28 DNLVLYE 34

```
RESULT 11
S39376
lectin - shallot
C:Species: Allium ascalonicum (shallot)
C:Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S39376
R:Mo, H.; van Damme, E.J.M.; Peumans, W.J.; Goldstein, I.T.
Arch. Biochem. Biophys. 306, 431-438, 1993
A:Title: Purification and characterization of a mannose-specific lectin from shallot (A1
A:Reference number: S39376; MUID:94029015; PMID:8215447
A:Accession: S39376
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-38 <MO>
A:Cross-references: UNIPROT:Q9S8Q9

Query Match
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 DNLVLYE 61
    |||||
Db 29 DNLVLYE 35

RESULT 12
WVWL
E7 protein - human papillomavirus type 1a
C:Species: human papillomavirus type 1a
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: C17475
R:Danos, O.; Karinka, M.; Yaniv, M.
EMBO J. 1, 231-236, 1982
A:Title: Human papillomavirus 1a complete DNA sequence: a novel type of genome organization
A:Reference number: A90970; MUID:84182467; PMID:6325156
A:Accession: C17475
A:Molecule type: DNA
A:Residues: 1-93 <DNA>
A:Cross-references: UNIPROT:P06465; GB:V01116; GB:X03321; NID:g60966; PIDN:CAA24316.1; F
R:Danos, O.; Engel, L.W.; Chen, E.Y.; Yaniv, M.; Howley, P.M.
J. Virol. 46, 557-566, 1993
A:Title: Comparative analysis of the human type 1a and bovine type 1 papillomavirus gene
A:Reference number: A92993; MUID:83189357; PMID:6302319
A:Contents: annotation
A:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 VQLRPS 218
    |||||
Db 12 VQLRPS 18

RESULT 13
G90536
hypothetical protein MYPU 1990 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: G90536
R:Hamoud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: G90536
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <KUR>
A:Cross-references: UNIPROT:Q98H11; GB:AL445566; PID:G14089612; PIDN:CA013372.1; GSPDB:G
A:Experimental source: strain UAB CTIP
```

```
C:Genetics:
A:Gene: MYPU 1990
A:Genetic code: SGC3

Query Match
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 LNTKNS 172
    |||||
Db 81 LNTKNS 87

RESULT 14
E75616
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: E75616
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M
S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; M
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: E75616
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-135 <WHI>
A:Cross-references: UNIPROT:Q9RYV9; GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF123
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0197
A:Map position: 2

Query Match
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VLLSGA 17
    |||||
Db 17 VLLSGA 23

RESULT 15
F75327
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: F75327
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M
S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; M
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: F75327
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149 <WHI>
A:Cross-references: UNIPROT:Q9RSV4; GB:AE002038; GB:AE000513; NID:g6459790; PIDN:AAF115
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2018
A:Map position: 1

Query Match
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LILSGA 18
    |||||
Db 47 LILSGA 53
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Thu Dec 16 12:21:14 2004

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Page 5

Search completed: December 15, 2004, 17:01:04  
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:38:47 ; Search time 196 Seconds

(without alignments)  
968.743 Million cell updates/sec

Title: US-09-868-605-14  
Perfect score: 330  
Sequence: 1 MGLSNILFWVLLSGAASL.....NLTASDDNDSTDEFLKSKL 330

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : uniprot\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                   |
|------------|-------|-------------|--------|-------|-------------------------------|
| 1          | 325   | 98.5        | 325    | 2     | 002838 sus scrofa             |
| 2          | 44    | 13.3        | 44     | 2     | 09GKT5 sus scrofa             |
| 3          | 19    | 5.8         | 93     | 2     | 06QW20 bos taurus             |
| 4          | 19    | 5.8         | 93     | 2     | AAG48374 AAG48374 bos tauru   |
| 5          | 19    | 5.8         | 284    | 2     | 09GLJ3 09GLJ3 bos taurus      |
| 6          | 14    | 4.2         | 329    | 2     | 09XGX6 09XGX6 felis silve     |
| 7          | 14    | 4.2         | 332    | 2     | 09GWM7 09GWM7 felis silve     |
| 8          | 14    | 4.2         | 332    | 2     | 09SL16 09SL16 felis silve     |
| 9          | 13    | 3.9         | 280    | 2     | 09TFF1 09TFF1 canis fami      |
| 10         | 13    | 3.9         | 329    | 2     | 09TFF2 09TFF2 canis fami      |
| 11         | 12    | 3.6         | 309    | 1     | CD86_MOUSE P42082 mus musculu |
| 12         | 12    | 3.6         | 309    | 2     | 091V77 091V77 mus musculu     |
| 13         | 12    | 3.6         | 309    | 2     | AAD25880 AAD25880 mus muscu   |
| 14         | 12    | 3.6         | 309    | 2     | AAD25881 AAD25881 mus muscu   |
| 15         | 12    | 3.6         | 309    | 2     | AAD25882 AAD25882 mus muscu   |
| 16         | 12    | 3.6         | 309    | 2     | AAD25883 AAD25883 mus muscu   |
| 17         | 12    | 3.6         | 309    | 2     | BAC37666 BAC37666 mus muscu   |
| 18         | 12    | 3.6         | 314    | 2     | 061238 061238 mus musculu     |
| 19         | 12    | 3.6         | 356    | 2     | 064381 064381 mus musculu     |
| 20         | 10    | 3.0         | 149    | 2     | 062810 062810 mus musculu     |
| 21         | 10    | 3.0         | 275    | 2     | 09BDN9 09BDN9 papio anubi     |
| 22         | 10    | 3.0         | 313    | 2     | 035531 035531 ratu            |
| 23         | 10    | 3.0         | 323    | 2     | 09BDB8 09BDB8 cercocebus      |
| 24         | 10    | 3.0         | 323    | 2     | 09BDM2 09BDM2 cercocebus      |
| 25         | 10    | 3.0         | 323    | 2     | 09BDM4 09BDM4 macaca mula     |
| 26         | 10    | 3.0         | 323    | 2     | 09BDM9 09BDM9 macaca neme     |
| 27         | 10    | 3.0         | 329    | 1     | CD86_HUMAN P42081 homo sapien |
| 28         | 10    | 3.0         | 329    | 1     | AHA40261 AHA40261 homo sapi   |
| 29         | 10    | 3.0         | 330    | 1     | P42071 oryctolagus            |
| 30         | 10    | 3.0         | 330    | 1     | CD86_RABIT O81224             |
| 31         | 8     | 2.4         | 108    | 2     | O81224 ralestonia s           |
|            |       |             | 250    | 2     | O88146 lacobacacili           |

ALIGNMENTS

| ID                                                           | 002838                                                                | PRELIMINARY;                                                     | PRT; | 325 AA. |
|--------------------------------------------------------------|-----------------------------------------------------------------------|------------------------------------------------------------------|------|---------|
| AC                                                           | 002838:                                                               |                                                                  |      |         |
| DI                                                           | 01-UTL-1997 (TREMBlrel. 04, Created)                                  |                                                                  |      |         |
| DT                                                           | 01-UTL-1997 (TREMBlrel. 04, Last sequence update)                     |                                                                  |      |         |
| DT                                                           | 01-OCT-2003 (TREMBlrel. 25, Last annotation update)                   |                                                                  |      |         |
| DE                                                           | B7-2.                                                                 |                                                                  |      |         |
| GN                                                           | Name=CD86;                                                            |                                                                  |      |         |
| OS                                                           | Sus scrofa (pig).                                                     |                                                                  |      |         |
| OC                                                           | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |                                                                  |      |         |
| OC                                                           | Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.                     |                                                                  |      |         |
| OX                                                           | NCB1_taxid=9623;                                                      |                                                                  |      |         |
| RN                                                           | [1]                                                                   |                                                                  |      |         |
| RP                                                           | SEQUENCE FROM N.A.                                                    |                                                                  |      |         |
| RX                                                           | MEDLINE=97047772; PubMed=8892613;                                     |                                                                  |      |         |
| RA                                                           | Maher S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,              |                                                                  |      |         |
| RA                                                           | Bothwell A.L.,                                                        |                                                                  |      |         |
| RT                                                           | "Porcine endothelial CD86 is a major costimulator of xenogeneic human |                                                                  |      |         |
| RT                                                           | T cells: cloning, sequencing, and functional expression in human      |                                                                  |      |         |
| RT                                                           | endothelial cells."                                                   |                                                                  |      |         |
| RL                                                           | J. Immunol. 157:3838-3844(1996).                                      |                                                                  |      |         |
| DR                                                           | EMBL: L76039; AAB61307.1; -.                                          |                                                                  |      |         |
| DR                                                           | HSSP: P42081; INCN                                                    |                                                                  |      |         |
| DR                                                           | InterPro: IPR007110; IG-like.                                         |                                                                  |      |         |
| DR                                                           | InterPro: IPR003596; IG_v.                                            |                                                                  |      |         |
| DR                                                           | Pfam: PF00047; IG_1.                                                  |                                                                  |      |         |
| DR                                                           | SMART: SM00406; IGv_1.                                                |                                                                  |      |         |
| DR                                                           | PROSITE: PS50835; IG_LIKE; 1.                                         |                                                                  |      |         |
| SQ                                                           | SEQUENCE 325 AA; 36527 MW; 98880813780597D CRC64;                     |                                                                  |      |         |
| Query Match 98.5%; Score 325; DB 2; Length 325;              |                                                                       |                                                                  |      |         |
| Best local Similarity 100.0%; Pred. No. 0;                   |                                                                       |                                                                  |      |         |
| Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                                                                       |                                                                  |      |         |
| QY                                                           | 1                                                                     | MGLSNILFWVLLSGAASLKSQAYFNETGELPCHFTNSQVLSIDELVIFWODQDNVLY 60     |      |         |
| DB                                                           | 1                                                                     | MGLSNILFWVLLSGAASLKSQAYFNETGELPCHFTNSQVLSIDELVIFWODQDNVLY 60     |      |         |
| QY                                                           | 61                                                                    | ELYRGOEKPHNVNSKYNIGRTSFDQATWTLRLHNVQIQDKSGYOCFHHKGGHGLVPIHOM 120 |      |         |
| DB                                                           | 61                                                                    | ELYRGOEKPHNVNSKYNIGRTSFDQATWTLRLHNVQIQDKSGYOCFHHKGGHGLVPIHOM 120 |      |         |
| QY                                                           | 121                                                                   | SSDSLILANFQPEINILNHTENSVINLTCSTQGYPEPORMMLANTKSTTEHDADM 180      |      |         |
| DB                                                           | 121                                                                   | SSDSLILANFQPEINILNHTENSVINLTCSTQGYPEPORMMLANTKSTTEHDADM 180      |      |         |
| QY                                                           | 121                                                                   | SSDSLILANFQPEINILNHTENSVINLTCSTQGYPEPORMMLANTKSTTEHDADM 180      |      |         |
| DB                                                           | 121                                                                   | SSDSLILANFQPEINILNHTENSVINLTCSTQGYPEPORMMLANTKSTTEHDADM 180      |      |         |
| QY                                                           | 181                                                                   | KKSQNNITELYNVSIKPSLPIPETNVSIVCVIQLIESKTLFSLPCNIDAKPPVQPPVP 240   |      |         |
| DB                                                           | 181                                                                   | KKSQNNITELYNVSIKPSLPIPETNVSIVCVIQLIESKTLFSLPCNIDAKPPVQPPVP 240   |      |         |
| QY                                                           | 241                                                                   | DHILMIALVTVVVGWMSFVTLRKRRKKQPPSPNECGETIIMNKKASQOTNRAEVH 300      |      |         |
| DB                                                           | 241                                                                   | DHILMIALVTVVVGWMSFVTLRKRRKKQPPSPNECGETIIMNKKASQOTNRAEVH 300      |      |         |

Qy 301 ERSDDACDVNLIKTSAPDNGTTDF 325  
 Db 301 ERSDDACDVNLIKTSAPDNGTTDF 325

## RESULT 2

Q9GKJ5 PRELIMINARY; PRT; 44 AA.  
 AC Q9GKJ5;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE Cosmimulatory B-lymphocyte antigen B7-2 (Fragment).  
 GN Name=CD86; (Pig).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9913;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21419000; PubMed=11528129;  
 RA Van Poucke M., Verle M., Tuglie C., Piumi F., Genet C.,  
 RT "Integration of porcine chromosome 13 maps."  
 RL Cytogenet. Cell Genet. 93:297-303(2001).  
 DR EMBL; AF222915; AAG41128.1; --  
 FT NON TER 1  
 FT NON TER 44  
 SQ SEQUENCE 44 AA; 5172 MW; 0721760B21759C CRC64;

Query Match 13.3%; Score 44; DB 2; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-36;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 157 YPEPQRMVLTNKTSTHEADMKSSONNITELYNISIRSLP 200  
 Db 1 YPEPQRMVLTNKTSTHEADMKSSONNITELYNISIRSLP 44

## RESULT 3

Q6QM20 PRELIMINARY; PRT; 93 AA.  
 AC Q6QM20;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DR CD86 (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Norimine J., Brown W.C.;  
 RL Submitted (Jan-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF533858; AAS48374.1; --  
 FT NON TER 1  
 FT NON TER 93  
 SQ SEQUENCE 93 AA; 10281 MW; 323B38A28889D6C3 CRC64;

Query Match 5.8%; Score 19; DB 2; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 237 PPVPDHIMIALVTVV 255  
 Db 6 PPVPDHIMIALVTVV 24

RESULT 4  
 AAS48374 PRELIMINARY; PRT; 93 AA.

AC AAS48374;  
 DT 10-MAR-2004 (TREMBLrel. 27, Created)  
 DT 10-MAR-2004 (TREMBLrel. 27, Last sequence update)  
 DT 10-MAR-2004 (TREMBLrel. 27, Last annotation update)  
 DE CD86 (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Norimine J., Brown W.C.;  
 RL "Bovine CD86 3'UTR."  
 DR EMBL; AF533858; AAS48374.1; --  
 FT NON TER 1  
 FT NON TER 1  
 SQ SEQUENCE 93 AA; 10281 MW; 323B38A28889D6C3 CRC64;

Qy 237 PPVPDHIMIALVTVV 255  
 Db 6 PPVPDHIMIALVTVV 24

Query Match 5.8%; Score 19; DB 2; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5  
 Q9GLJ3 PRELIMINARY; PRT; 284 AA.  
 AC Q9GLJ3;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE CD86 antigen (Fragment).  
 GN Name=CD86;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Tissue=Peripheral blood;  
 RA Brooke G.P., Howard C.J., Parsons K.R.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ291475; CAC13140.1; --  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGv\_1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON TER 284  
 FT NON TER 284  
 SQ SEQUENCE 284 AA; 32021 MW; 797BB6639E297841 CRC64;

Query Match 5.8%; Score 19; DB 2; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 237 PPVPDHIMIALVTVV 255  
 Db 251 PPVPDHIMIALVTVV 269

RESULT 6  
 Q9XSX6 PRELIMINARY; PRT; 329 AA.  
 AC Q9XSX6;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE CD86 antigen.

GN Name=CD86;  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20180222; PubMed=10711336;  
 RA Choi I.S., Hash S.M., Winslow B.J., Collisson E.W.;  
 RT "Sequence analyses of feline B7 costimulatory molecules.";  
 RL Vet. Immunol. Immunopathol. 73:219-231(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Choi I.S., Hash S., Winslow B.J., Collisson E.W.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF157827; AAD42974.1; -.  
 DR HSSP; P42081; INCN.  
 DR InterPro; IPR007110; IG-like.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IGV; 1.  
 SQ SEQUENCE 329 AA; 37481 MW; A10621E3C00A08BB CRC64;

Query Match 4.2%; Score 14; DB 2; Length 329;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLLRHNVQIKDKG 100  
 DB 94 WTLLRHNVQIKDKG 107

RESULT 7  
 ID 09GMZ7 PRELIMINARY; PRT; 332 AA.  
 AC 09GMZ7;  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE B-lymphocyte activation antigen B7-2 (CD86).  
 GN Name=CD86;  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20485322; PubMed=11029611;  
 RA Mishimura Y., Shimojima M., Miyazawa T., Sato E., Nakamura K.,  
 RA Isumiya Y., Ikeda Y., Mikami T., Takahashi E.;  
 RT "Molecular cloning of the cDNA encoding the feline B-lymphocyte  
 RT activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which  
 RT interact with human CTLA-4-1g.";  
 RL Eur. J. Immunogenet. 27:427-430(2000).  
 DR EMBL; AB030652; BAB11688.1; -.  
 DR HSSP; P42081; INCN.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IGV; 1.  
 SQ SEQUENCE 332 AA; 37812 MW; 672C9B367D1E3C0 CRC64;

Query Match 4.2%; Score 14; DB 2; Length 332;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLLRHNVQIKDKG 100  
 DB 94 WTLLRHNVQIKDKG 107

RESULT 8  
 Q95LI6

ID Q95LI6 PRELIMINARY; PRT; 332 AA.  
 AC Q95LI6;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE CD86.  
 GN Name=CD86;  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21390213; PubMed=11498243;  
 RA Yang S., Sellins K.S., Powell T., Stoneman E., Sim G.K.;  
 RT "Novel transcripts encoding secreted forms of feline CD80 and CD86  
 RT costimulatory molecules.";  
 RL Vet. Immunol. Immunopathol. 81:15-21(2001).  
 DR EMBL; AY007704; AAG23342.1; -.  
 DR HSSP; P42081; INCN.  
 DR InterPro; IPR007110; IG-like.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IGV; 1.  
 SQ SEQUENCE 332 AA; 37826 MW; 8BFC9B367D1E3D8 CRC64;

Query Match 4.2%; Score 14; DB 2; Length 332;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLLRHNVQIKDKG 100  
 DB 94 WTLLRHNVQIKDKG 107

RESULT 9  
 ID Q9TFL PRELIMINARY; PRT; 280 AA.  
 AC Q9TFL;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Truncated B7-2 protein.  
 GN Name=CD86;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20093996; PubMed=10630300;  
 RA Yang S., Sim G.K.,  
 RT "New forms of dog CD80 and CD86 transcripts that encode secreted B7  
 RT molecules.";  
 RL Immunogenetics 50:349-353(1999).  
 DR EMBL; AF106827; AAF17298.1; -.  
 DR HSSP; P42081; INCN.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IGH.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IGV; 1.  
 DR PROSITE; PS00290; IGHMC; UNKNOWN 1.  
 SQ SEQUENCE 280 AA; 32265 MW; 3CEBCA4D826A7F3 CRC64;

Query Match 3.9%; Score 13; DB 2; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 0.0004;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TGEPLCHFTNSGN 41  
 DB 35 TGEPLCHFTNSGN 47

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RESULT 10
Q9TF2 PRELIMINARY; PRT; 329 AA.
AC Q9TF2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TREMBLrel. 26, Last annotation update)
DE B7-2 protein.
GN Name=CD86;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20093996; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New forms of dog CD80 and CD86 transcripts that encode secreted B7
RT molecules.";
RL Immunogenetics 50:349-353(1999).
DR EMBL; AF106825; AAF17297.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 329 AA; 37774 MW; D98B83437B7B73 CRC64;

Query Match 3.6%; Score 13; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TGELEPCHFTNSON 41
DB 35 TGELEPCHFTNSON 47

RESULT 11
CD86_MOUSE STANDARD; PRT; 309 AA.
AC P42082;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE T lymphocyte activation antigen CD86 precursor (Activation B7-2
DE antigen) (Early T cell costimulatory molecule-1) (Etc-1).
GN Name=CD86;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94055585; PubMed=7504059;
RA Freeman G.J., Borriello F., Hodas R.J., Reiser H., Gibben J.G.,
RA Ng J.W., Kim J., Goldberg J.M., Hancock K., Laszlo G., Lombard L.A.,
RA Wang S., Gray G.S., Nadler L.M., Sharpe A.H.;
RT "Murine B7-2, an alternative CTLA4 counter-receptor that costimulates
RT T cell proliferation and interleukin 2 production.";
RL J. Exp. Med. 178:2185-2192(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129;
RC MEDLINE=96094437; PubMed=7499829;
RA Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;
RT "Differential expression of alternate mB7-2 transcripts.";
RL J. Immunol. 155:5490-5497(1995).
RN [3]
RP SEQUENCE OF 7-309 FROM N.A.
RX MEDLINE=94230971; PubMed=7513726;

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RA Chen C., Gault A., Shen L., Nabavi N.;
RT "Molecular cloning and expression of early T cell costimulatory
RT molecule-1 and its characterization as B7-2 molecule.";
RL J. Immunol. 152:4929-4936(1994).
CC -1- FUNCTION: Receptor involved in the costimulatory signal essential
CC for T lymphocyte proliferation and interleukin 2 production, by
CC binding CD28 or CTLA-4. May play a critical role in the early
CC events of T cell activation and costimulation of naive T cells,
CC such as deciding between immunity and anergy that is made by T
CC cells within 24 hours after activation.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed on activated B cells.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-7 is the initiator.
CC -----
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DR EMBL; U39848; AAC52334.1; JOINED.
DR EMBL; U39849; AAC52334.1; JOINED.
DR EMBL; U39850; AAC52334.1; JOINED.
DR EMBL; U39851; AAC52334.1; JOINED.
DR EMBL; U39852; AAC52334.1; JOINED.
DR EMBL; U39853; AAC52334.1; JOINED.
DR EMBL; U39854; AAC52334.1; JOINED.
DR EMBL; U39855; AAC52334.1; JOINED.
DR EMBL; U39856; AAC52334.1; JOINED.
DR EMBL; U39857; AAC52334.1; JOINED.
DR EMBL; U39858; AAC52334.1; JOINED.
DR EMBL; U39859; AAC52334.1; JOINED.
DR EMBL; U39860; AAC52334.1; JOINED.
DR EMBL; U39861; AAC52334.1; JOINED.
DR EMBL; U39862; AAC52334.1; JOINED.
DR EMBL; U39863; AAC52334.1; JOINED.
DR EMBL; U39864; AAC52334.1; JOINED.
DR EMBL; U39865; AAC52334.1; JOINED.
DR EMBL; U39866; AAC52334.1; JOINED.
DR EMBL; U39867; AAC52334.1; JOINED.
DR EMBL; U39868; AAC52334.1; JOINED.
DR EMBL; U39869; AAC52334.1; JOINED.
DR EMBL; U39870; AAC52334.1; JOINED.
DR EMBL; U39871; AAC52334.1; JOINED.
DR EMBL; U39872; AAC52334.1; JOINED.
DR EMBL; U39873; AAC52334.1; JOINED.
DR EMBL; U39874; AAC52334.1; JOINED.
DR EMBL; U39875; AAC52334.1; JOINED.
DR EMBL; U39876; AAC52334.1; JOINED.
DR EMBL; U39877; AAC52334.1; JOINED.
DR EMBL; U39878; AAC52334.1; JOINED.
DR EMBL; U39879; AAC52334.1; JOINED.
DR EMBL; U39880; AAC52334.1; JOINED.
DR EMBL; U39881; AAC52334.1; JOINED.
DR EMBL; U39882; AAC52334.1; JOINED.
DR EMBL; U39883; AAC52334.1; JOINED.
DR EMBL; U39884; AAC5233
```

QY 87 WTLRLHNVQIKD 98  
 DB 93 WTLRLHNVQIKD 104

## RESULT 12

Q91YV7 PRELIMINARY; PRT; 309 AA.  
 AC Q91YV7;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE CD86 antigen.  
 GN Name=CD86;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.  
 RC Expression driven by an MMTV-LTR enhancer;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares W.B., Bonaldo W.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullanbly S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.T., Hulik S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
 Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,  
 Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.  
 RC Expression driven by an MMTV-LTR enhancer;  
 RA Strausberg R., et al. (2001) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC013807; AAH13807.1; -  
 DR HSSP; P42081; INCN.  
 DR MGD; MGI:101773; Cd86.  
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 SQ SEQUENCE 309 AA; 34713 MW; 61593C49FECB0CES CRC64;

Query Match 3.6%; Score 12; DB 2; Length 309;  
 Best Local Similarity 100.0%; Pred.No. 0.0045;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKD 98  
 DB 93 WTLRLHNVQIKD 104

## RESULT 13

AAD25880

ID AAD25880 PRELIMINARY; PRT; 309 AA.

AC AAD25880;  
 DT 02-MAR-2004 (TREMBLrel. 27, Created)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)  
 DE CD86 antigen.  
 GN CD86.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A/J; TISSUE=spleen;  
 RA Ma R.Z., Teuscher C.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF065897; AAD25880.1; -  
 SQ SEQUENCE 309 AA; 34665 MW; 8F58DCD1FB81D5EA CRC64;

Query Match 3.6%; Score 12; DB 2; Length 309;  
 Best Local Similarity 100.0%; Pred.No. 0.0045;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKD 98  
 DB 93 WTLRLHNVQIKD 104

## RESULT 14

AAD25881 PRELIMINARY; PRT; 309 AA.  
 AC AAD25881;  
 DT 02-MAR-2004 (TREMBLrel. 27, Created)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)  
 DE CD86 antigen.  
 GN CD86.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=spleen;  
 RA Ma R.Z., Teuscher C.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF065898; AAD25881.1; -  
 SQ SEQUENCE 309 AA; 34665 MW; 8F58DCD1FB81D5EA CRC64;

Query Match 3.6%; Score 12; DB 2; Length 309;  
 Best Local Similarity 100.0%; Pred.No. 0.0045;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKD 98  
 DB 93 WTLRLHNVQIKD 104

## RESULT 15

AAD25882 PRELIMINARY; PRT; 309 AA.  
 AC AAD25882;  
 DT 02-MAR-2004 (TREMBLrel. 27, Created)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)  
 DE CD86 antigen.  
 GN CD86.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=B10.S/J; TISSUE=spleen;  
 RA Ma R 2, Teuscher C; to the EMBL/GenBank/DBJ databases.  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF065899; AAD25882.1; -  
 SQ SEQUENCE 309 AA; 3465 MW; 8F58DDC1FB8ID5EA CRC64;  
 Query Match 3.6%; Score 12; DB 2; Length 309;  
 Best Local Similarity 100.0%; Pred.No. 0.0045;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 87 WTLRLHNVQIKD 98  
 |||||  
 Db 93 WTLRLHNVQIKD 104  
 |||||

Search completed: December 15, 2004, 17:00:18  
 Job time : 199 secs